GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 00:41:05 ; Search time 9096.67 Seconds
(without alignments)
12582.818 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
Sequence: 1 ctatctcctctctcagccgc.....ttaaaaaaaaaaaaaaaaa 3833

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	986	25.7	1798	11	AF125103	AF125103 Homo sapi
	2	915.6	23.9	1785	11	AF077050	AF077050 Homo sapi
	3	774.2	20.2	3533	11	AK034902	AK034902 Mus muscu
c	4	668.6	17.4	956	9	AL573494	AL573494 AL573494
	5	646.8	16.9	896	14	CB204418	CB204418 AGENCOURT
	6	642	16.7	1003	14	CK231727	CK231727 ILLUMIGEN
	7	634.2	16.5	1101	14	CF110956	CF110956 Shultzomi
	8	631	16.5	871	13	BQ719894	BQ719894 AGENCOURT
	9	628.8	16.4	646	14	CB467517	CB467517 733269 MA
	10	625.4	16.3	627	12	BM986175	BM986175 LM24HW001
	11	621.4	16.2	843	12	BG570231	BG570231 602590632
	12	619	16.1	619	14	CF768055	CF768055 CES004952
	13	618.6	16.1	1164	14	CK232009	CK232009 ILLUMIGEN
	14	617	16.1	631	10	BF044381	BF044381 BP250021B
	15	614.2	16.0	822	14	CB521332	CB521332 UI-M-GH0-
	16	605.2	15.8	901	13	BQ879359	BQ879359 AGENCOURT
	17	591.4	15.4	593	10	BF039928	BF039928 BP250015A
c	18	588.8	15.4	606	14	CF765999	CF765999 CES000103
	19	587	15.3	587	12	BI775114	BI775114 467491 MA
	20	581.2	15.2	958	12	BM801698	BM801698 AGENCOURT
c	21	580	15.1	996	10	BF570468	BF570468 602186269
	22	572.6	14.9	969	12	BG706140	BG706140 602669409
c	23	568.8	14.8	598	14	CB534701	CB534701 768054 MA
	24	568.8	14.8	730	12	BI601346	BI601346 603245090
	25	567.6	14.8	986	13	BU841009	BU841009 AGENCOURT
	26	566	14.8	882	13	BQ233389	BQ233389 AGENCOURT
	27	565	14.7	579	14	CB222263	CB222263 1IL25H09
	28	564.8	14.7	819	12	BG109465	BG109465 602280543
	29	564	14.7	772	14	CF948588	CF948588 UI-M-HJ0-
	30	564	14.7	842	13	BU709149	BU709149 UI-M-EW0-
	31	562	14.7	1022	12	BM557554	BM557554 AGENCOURT
c	32	560.8	14.6	783	12	BQ001312	BQ001312 UI-H-DH1-
	33	558.8	14.6	598	14	CF118424	CF118424 fs543.z1
c	34	558	14.6	789	13	BU619407	BU619407 UI-H-FL1-
c	35	557.8	14.6	586	14	CB534657	CB534657 768008 MA
	36	557.4	14.5	578	14	CF762449	CF762449 CES000069
	37	557.2	14.5	845	9	AL533461	AL533461 AL533461
	38	556.8	14.5	707	14	CF793493	CF793493 888888 MA
	39	556.8	14.5	954	12	BM470283	BM470283 AGENCOURT
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	41	556.2	14.5	650	14	CB215381	CB215381 NISC_np05
	42	556	14.5	556	10	BF039736	BF039736 BP250014B
	43	553	14.4	699	12	BG819566	BG819566 602783209
	44	552.6	14.4	758	12	BG697436	BG697436 602660623
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ALIGNMENTS

RESULT 1
AF125103
LOCUS AF125103 1798 bp mRNA linear HTC 22-MAY-2001
DEFINITION Homo sapiens neuroendocrine specific protein c homolog mRNA, complete cds.
ACCESSION AF125103
VERSION AF125103.1 GI:5107001
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1798)
AUTHORS Zhang,Q.H., Ye,M., Wu,X.Y., Ren,S.X., Zhao,M., Zhao,C.J., Fu,G., Shen,Y., Fan,H.Y., Lu,G., Zhong,M., Xu,X.R., Han,Z.G., Zhang,J.W., Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J. and Chen,Z.
TITLE Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells
JOURNAL Genome Res. 10 (10), 1546-1560 (2000)
MEDLINE 20499367
PUBMED 11042152
REFERENCE 2 (bases 1 to 1798)
AUTHORS Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H., Dai,M., Huang,Q., Chen,S. and Chen,Z.
TITLE Human neuroendocrine specific protein c homolog mRNA, complete cds
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1798)
AUTHORS Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H., Dai,M., Huang,Q., Chen,S. and Chen,Z.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P. R. China
FEATURES Location/Qualifiers
source 1. .1798
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="CD34+ hematopoietic stem/progenitor cells"
CDS 215. .814
/codon_start=1
/product="neuroendocrine specific protein c homolog"
/protein_id="AAD39920.1"
/db_xref="GI:5107002"
/translation="MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIV
SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA
LGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLLQCSC
YLERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"
ORIGIN

Query Match 25.7%; Score 986; DB 11; Length 1798;

Best Local Similarity 86.1%; Pred. No. 2.4e-169;
Matches 1360; Conservative 0; Mismatches 140; Indels 80; Gaps 21;

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Qy       2304 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 2363
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Db        248 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 307

Qy       2364 TTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
              | ||||||||||| ||  |||||||||||||||||||||| ||||| ||||||||||||
Db        308 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 367

Qy       2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
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Db        368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 427

Qy       2484 CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
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Db        428 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 487

Qy       2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAA 2603
             ||||||||||||||||||||||| |||||||||||||||||| |||||||| |||||
Db        488 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 547

Qy       2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 2663
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Db        548 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 607

Qy       2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT 2723
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Db        608 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 667

Qy       2724 CTGATTTCACT-CTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCA 2782
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Db        668 CTCATTTCACTCCTTCAGTGTTCCTGTTATTTA-GAACGGCATCAGGCACAGATAGATCA 726

Qy       2783 TTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAT 2842
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Qy       2843 CCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTT 2902
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Db        787 CCCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTT 841

Qy       2903 TATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCT 2962
              |||||||||||||||||||||||||  |  |||||||||||||||||| || |||
Db        842 CATCTTTAAAGGGGATATTCATTTGATTATACGGGGGAGGGTCAGGGAAGAACGAA-CCT 900

Qy       2963 TGACATTGCAGTGCAGTTTCAC----------AGATCTTTATTTTTAGCAACGCAGTG- 3010
             ||||  ||||||||||||||||          |||||||||||||||| | ||| ||
Db        901 TGACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTTAGCCATGCACTGT 960

Qy       3011 TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGTAAGCT 3070
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Db        961 TGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTTCATCATCTTAAGTATTGTAAGCT 1020

Qy       3071 GCTATGTATGGATTTAAATCGTAATCATATTTGTTT--TTCCTGTATGAGGCACTGGTGA 3128
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Db        1021 GCTATGTATGGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACTGGTGG 1080

Qy        3129 ATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGTAT- 3187
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Db        1081 AATAAAAAAC-----------CTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATC 1129

Qy        3188 TTGGGGAATTGCAAAGAAAGTGGAGCT------GACAGAAATAACCCTTTTCACAGTTTG 3241
               ||||  | |||||  |||  ||||||||       | | |||  ||  |  ||  |||||||
Db        1130 TTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTG 1189

Qy        3242 TGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAA----TGTTTAG 3297
               ||||||||||| |||| ||||||  ||||||||||||||||||||||||    |||||||
Db        1190 TGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTGTTTAG 1249

Qy        3298 ACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGT 3357
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Db        1250 ACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGT 1308

Qy        3358 GTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATAT 3417
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Db        1309 GTATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGTAAATATAGATTATA----- 1363

Qy        3418 CTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTG 3477
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Db        1364 -TATGTATAGTGTTTCACAAAGCTTAGACCTTTACCTT-CCAGCCACCCCACAGTGCTTG 1421

Qy        3478 ATACT------TCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAG 3531
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Db        1422 ATATTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAAGA 1481

Qy        3532 AAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAG 3591
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Db        1482 AGAAATATTTCTAGGAGCACTACCATC-GTTTTCAACATGAA---ATGCCACACACATAG 1537

Qy        3592 AACTCC-TCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACA--AAC 3648
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Db        1538 AACTCCAACAACATCAATTTCATTGCACAGACTGACTGTAGTTAATTTTGTCACAGGATC 1597

Qy        3649 TCTGGACTGAATCTAATGCTTCCAAAAA-------TGTTTGCAAATATCAAACATTGTTA 3701
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Db        1598 TATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTTTGCAAATATCAAACATTGTTA 1657

Qy        3702 TGTAAGAAAATAT--------AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGA 3753
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Db        1658 TGCAAGAAATTATTAATTACAAAATGAAGATTTATACCATTGTGGTTTAAGCTGTACTGA 1717

Qy        3754 ACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGAC 3813
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Db        1718 ACTAAATCTGTGGAAGGCATTGTAAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGAC 1777

Qy        3814 TTAAAAAAAAAAAAAAAAAA 3833
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Db        1778 CCAAAACGAAAAAAAAAAAA 1797
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RESULT 2
AF077050

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LOCUS       AF077050                1785 bp    mRNA    linear   HTC 21-NOV-2002
DEFINITION  Homo sapiens neuroendocrine-specific protein C homolog mRNA,
            complete cds.
ACCESSION   AF077050
VERSION     AF077050.1  GI:4689147
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1785)
  AUTHORS   Song,H., Peng,Y., Zhou,J., Huang,Q., Dai,M., Mao,Y., Yu,Y., Xu,X.,
            Luo,B., Hu,R. and Chen,J.
  TITLE     Human neuroendocrine-specific protein C (NSP) homolog gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1785)
  AUTHORS   Song,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-1998) Rui-Jin Hospital, Shanghai Institute of
            Endocrinology, Molecular Medical Center, 197 Rui-Jin Road II,
            Shanghai 200025, P.R. China
FEATURES             Location/Qualifiers
     source          1. .1785
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                     /codon_start=1
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ORIGIN
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Query Match 23.9%; Score 915.6; DB 11; Length 1785;
Best Local Similarity 85.5%; Pred. No. 1.5e-156;
Matches 1238; Conservative 0; Mismatches 144; Indels 66; Gaps 17;

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Qy       2304 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 2363
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Db        247 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 306

Qy       2364 TTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
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Db        307 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 366

Qy       2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
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Db        367 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 426

Qy       2484 CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
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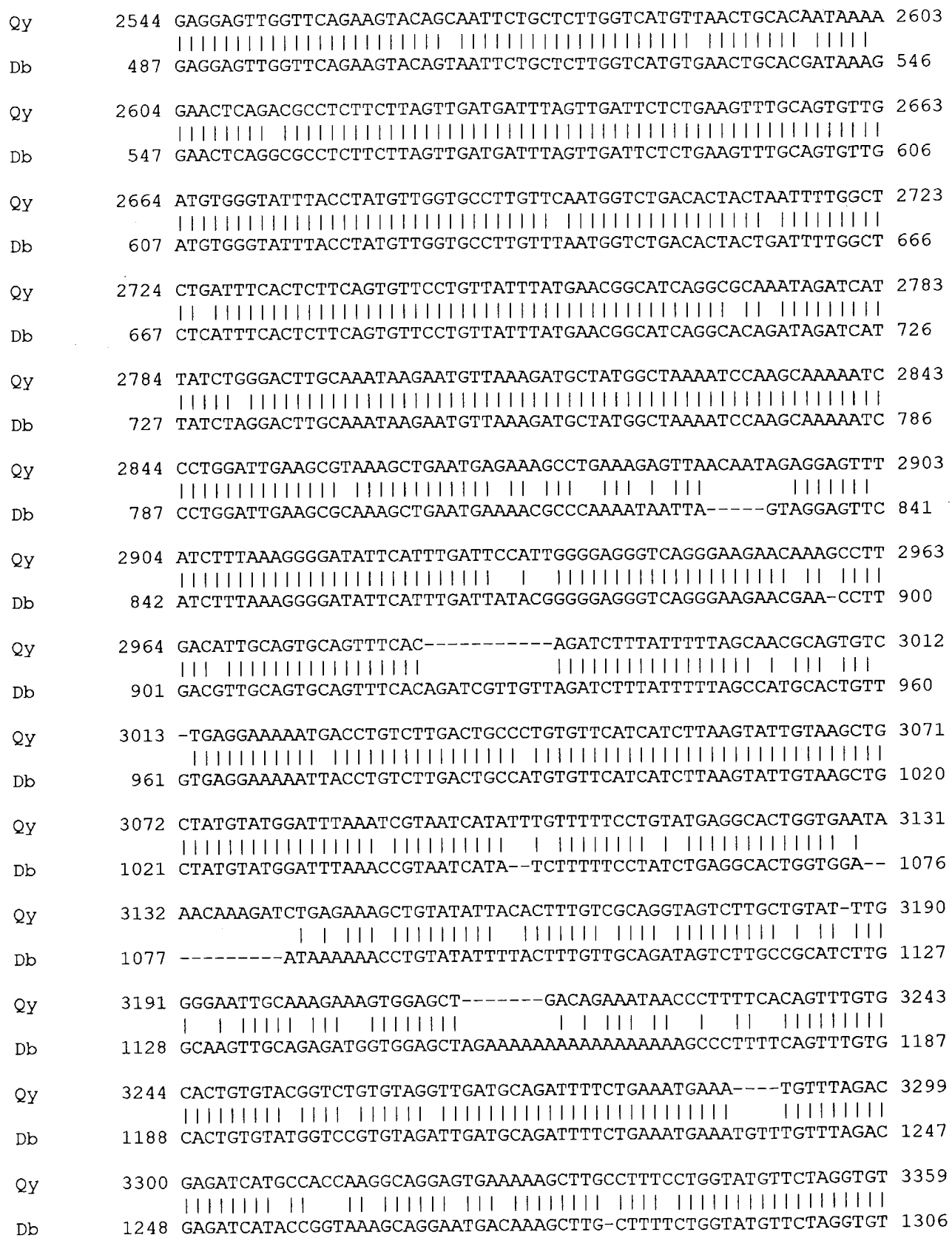

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Db       1307 ATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGTAAATATAGATTATATATG--- 1363

Qy       3420 ATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGAT 3479
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Db       1364 ---TATAGTGTTTCACAAAGCTTAGACCTTTACCTT-CCAGCCACCCCACAGTGCTTGAT 1419

Qy       3480 ACT------TCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAA 3533
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Db       1420 ATTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAAGAAG 1479

Qy       3534 ACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAA 3593
              |  || ||||||| |||||||||||||||||||||| |||   | ||||  || | ||||
Db       1480 AAATATTTCTAGGAGCACTACCATCTGTTTTCAACATGAA---ATGCCACACACATAGAA 1536

Qy       3594 CTCC-TCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCT- 3651
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Db       1537 CTCCAACAACATCAATTTCATTGCACAGACTGACTGTAGTTAATTTTGTCACAGAATCTA 1596

Qy       3652 GGACTGAATCTAATGCTTCCAAAA----ATGTTTGCAAATATCAAACATTGTTATGTAAG 3707
               | |||||||||||||| | ||||     | | |   ||   | ||||||||||||  ||
Db       1597 TGGCTGAATCTAATGCTCCAAAAATGTTGTTTGTTGCAAATACCAACATTGTTATGCCAG 1656

Qy       3708 AAAATATA 3715
              ||| | ||
Db       1657 AAATTTTA 1664
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RESULT 3
AK034902
LOCUS       AK034902               3533 bp    mRNA    linear   HTC 18-SEP-2003
DEFINITION  Mus musculus 12 days embryo embryonic body between diaphragm region
            and neck cDNA, RIKEN full-length enriched library, clone:9430059L06
            product:RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOGO PROTEIN)
            (FOOCEN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog [Rattus
            norvegicus], full insert sequence.
ACCESSION   AK034902
VERSION     AK034902.1  GI:26084268
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
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PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3533)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES Location/Qualifiers
source 1. .3533
/organism="Mus musculus"

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                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:9430059L06"
                     /db_xref="MGI:2399112"
                     /db_xref="taxon:10090"
                     /clone="9430059L06"
                     /tissue_type="embryonic body between diaphragm region and
                     neck"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="12 days embryo"
     misc_feature    1. .3533
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                     PROTEIN) (FOOCEN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog
                     [Rattus norvegicus] (SWISSPROT|Q9JK11, evidence: FASTY,
                     95.8%ID, 100%length, match=1068)"
ORIGIN

  Query Match             20.2%;  Score 774.2;  DB 11;  Length 3533;
  Best Local Similarity   78.3%;  Pred. No. 6.6e-131;
  Matches 1190;  Conservative    0;  Mismatches  258;  Indels   71;  Gaps   19;

Qy       2304 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 2363
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Db        740 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 799

Qy       2364 TTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
             || |||||||||||| || |||||||| |||||||||| ||||||||||||||||||||||
Db        800 TTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 859

Qy       2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        860 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATC 919

Qy       2484 CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
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Db        920 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA 979

Qy       2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAA 2603
             ||||| |||||||||||| || || |||||||||||||||||||| ||| ||||||||||||
Db        980 GAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 1039

Qy       2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 2663
             ||| | || || |||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1040 GAATTGAGGCGTCTCTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 1099

Qy       2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT 2723
             ||||| |||||||| || |||||||||||||||||||| |||||||||| ||||| |||
Db       1100 ATGTGAGTATTTACTTACGTTGGTGCCTTGTTCAATGGTTTGACACTACTGATTTTAGCT 1159

Qy       2724 CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
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Db       1160 CTGATCTCACTCTTCAGTATTCCTGTTATATATGAACGGCATCAGGCGCAGATAGATCAT 1219

Qy       2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
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Db       1220 TATCTAGGACTTGCAAACAAGAGCGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 1279
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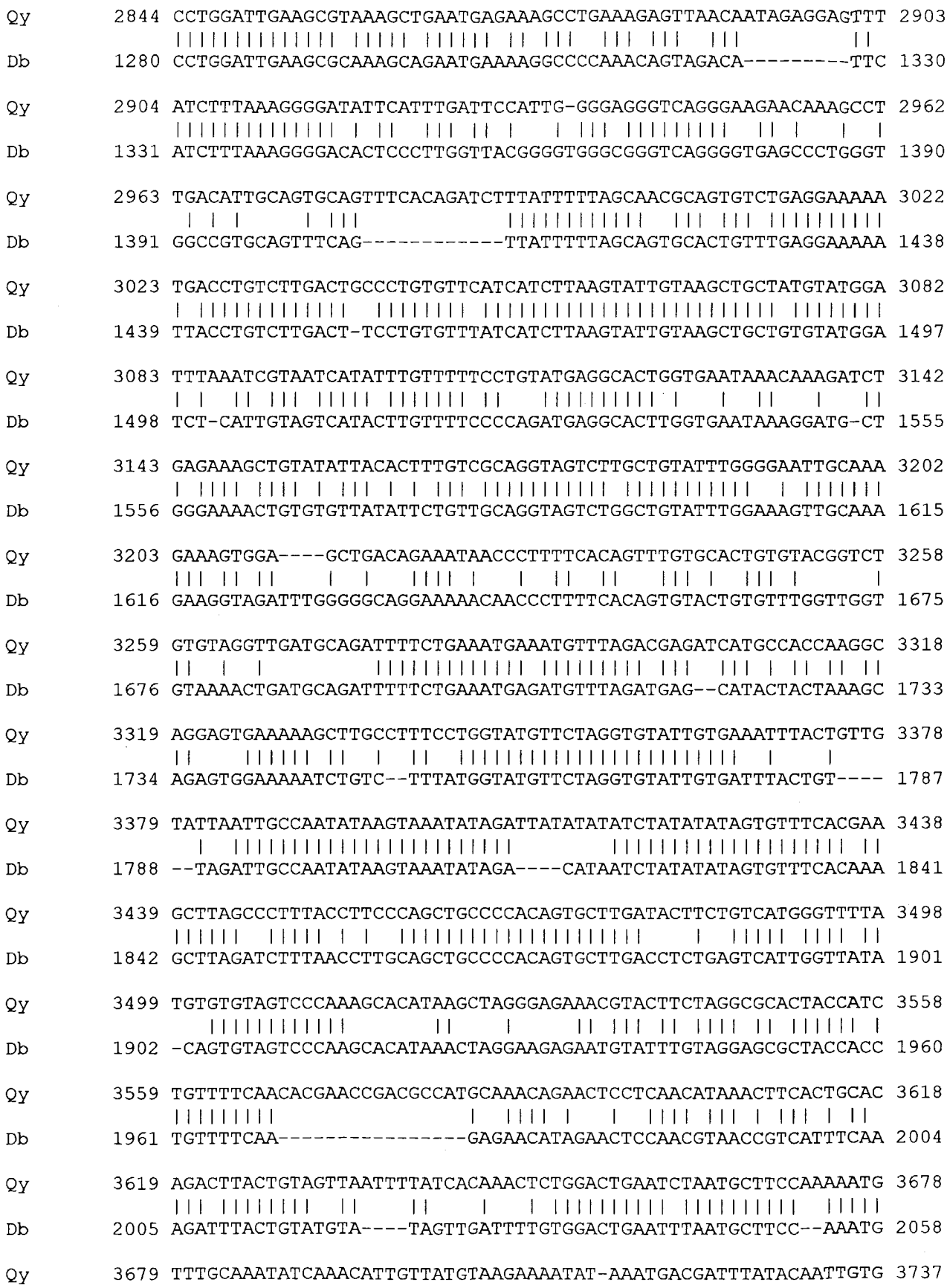

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Db       2059 TTTGCAGTTACCAAACATTGTTATGCAAGAAATCATAAAATGAAGACTTATACCATTGT- 2117

Qy       3738 GTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATC 3797
              |||||||||||||||| |  |||||||||||||||||||||||| ||||||||||||
Db       2118 GTTTAAGCTGTATTGAATT--ATCTGTGGAATGCATTGTGAACTGT-AAAGCAAAGTATC 2174

Qy       3798 AATAAAGCTTATAGACTTA 3816
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Db       2175 AATAAAGCTTATAGACTTA 2193
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RESULT 4
AL573494/c

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LOCUS       AL573494                956 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL573494 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI051YB11 3-PRIME, mRNA sequence.
ACCESSION   AL573494
VERSION     AL573494.2  GI:31294840
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 956)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12932794.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1423.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI051CA06NP1&cluster=1423.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI051CA06NP1.
FEATURES             Location/Qualifiers
     source          1. .956
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                     /db_xref="taxon:9606"
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                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

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  Query Match             17.4%;  Score 668.6;  DB 9;  Length 956;
  Best Local Similarity   88.7%;  Pred. No. 1.5e-111;
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Qy       2304 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 2363
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        878 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 819

Qy       2364 TTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
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Db        818 CTATTCCTGCTGCTTTCATTRACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 759

Qy       2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
              |||||||||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        758 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 699

Qy       2484 CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
              |||||||| |||||||||||||||||||||||| ||||||||||||||||||||||||
Db        698 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 639

Qy       2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAA 2603
              |||||||||||||||||||||| |||||||||||||||||| |||||||| |||||
Db        638 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 579

Qy       2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 2663
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Db        578 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 519

Qy       2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT 2723
              |||||||||||||||||||||||||||||| |||||||||||||||| |||||||||
Db        518 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 459

Qy       2724 CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
              || ||||||||||||||||||||||||||||||||||||||||||| || |||||||||
Db        458 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 399

Qy       2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 339

Qy       2844 CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT 2903
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Db        338 CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTC 284

Qy       2904 ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTT 2963
              |||||||||||||||||||||||||  | ||||||||||||||||||| || ||||
Db        283 ATCTTTAAAGGGGATATTCATTTGATTATACGGGGGAGGGTCAGGGAAGAACGAA-CCTT 225

Qy       2964 GACATTGCAGTGCAGTTTCAC----------AGATCTTTATTTTTAGCAACGCAGTG-T 3011
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Db        224 GACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTTAGCCATGCACTGTT 165

Qy       3012 CTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGTAAGCTG 3071
               |||||||||| ||||||||| |||||| |||||||||||||||||||||||||||||
Db        164 GTGAGGAAAAATTACCTGTCTTTACTGCCATGTGTTCATCATCTTAAGTATTGTAAGCTG 105

Qy       3072 CTATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATA 3131
              |||||||||||||||| ||:|||||||  | |||||||| | |||||||||||| |
Db        104 CTATGTATGGATTTAAACCGYAATCATA--TCTTTTTCCTATCTGAGGCACTGGTGGA-- 49
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Qy       3132 AACAAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGTAT 3187
                  | | ||| ||| | |||     |||||||| ||||| || | :|
Db         48 ---------ATAAAAAACCTGNANATTNNNACTTGTCGCAGATAGTCTGGCCGCMT 2


RESULT 5
CB204418
LOCUS       CB204418                 896 bp    mRNA    linear   EST 05-FEB-2003
DEFINITION  AGENCOURT_11276017 NIH_MGC_135 Mus musculus cDNA clone
            IMAGE:30138586 5', mRNA sequence.
ACCESSION   CB204418
VERSION     CB204418.1  GI:28241848
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 896)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. David Rowe
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM0041  row: k  column: 11
            High quality sequence stop: 686.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
                     /clone="IMAGE:30138586"
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                     /clone_lib="NIH_MGC_135"
                     /note="Vector: pCMVSport6.1; Site_1: EcoRV; Site_2: NotI;
                     Normalized full-length enriched library from pooled mouse
                     embryonic limb, maxilla and mandible, day 12.5, 13.5,
                     14.5, and 15.5 (size selected for the 0.5-1 kb fragments)
                     Cloned directionally, priming method: Oligo-dT. cDNA
                     enrichment: >1k bp, Average insert size 1.6k bp.
                     Normalization (Cot value): 7.5 kb. Priming sequence:
                     5'GACTAGTTCTAGATCGCGAGCGGCCGCCC(T)3' Tissue contributed
                     by, David Rowe. Library constructed by ResGen, Invitrogen
                     Corp."
ORIGIN

  Query Match             16.9%;  Score 646.8;  DB 14;  Length 896;
  Best Local Similarity   85.3%;  Pred. No. 1.4e-107;
  Matches  761;  Conservative    0;  Mismatches  117;  Indels   14;  Gaps    3;
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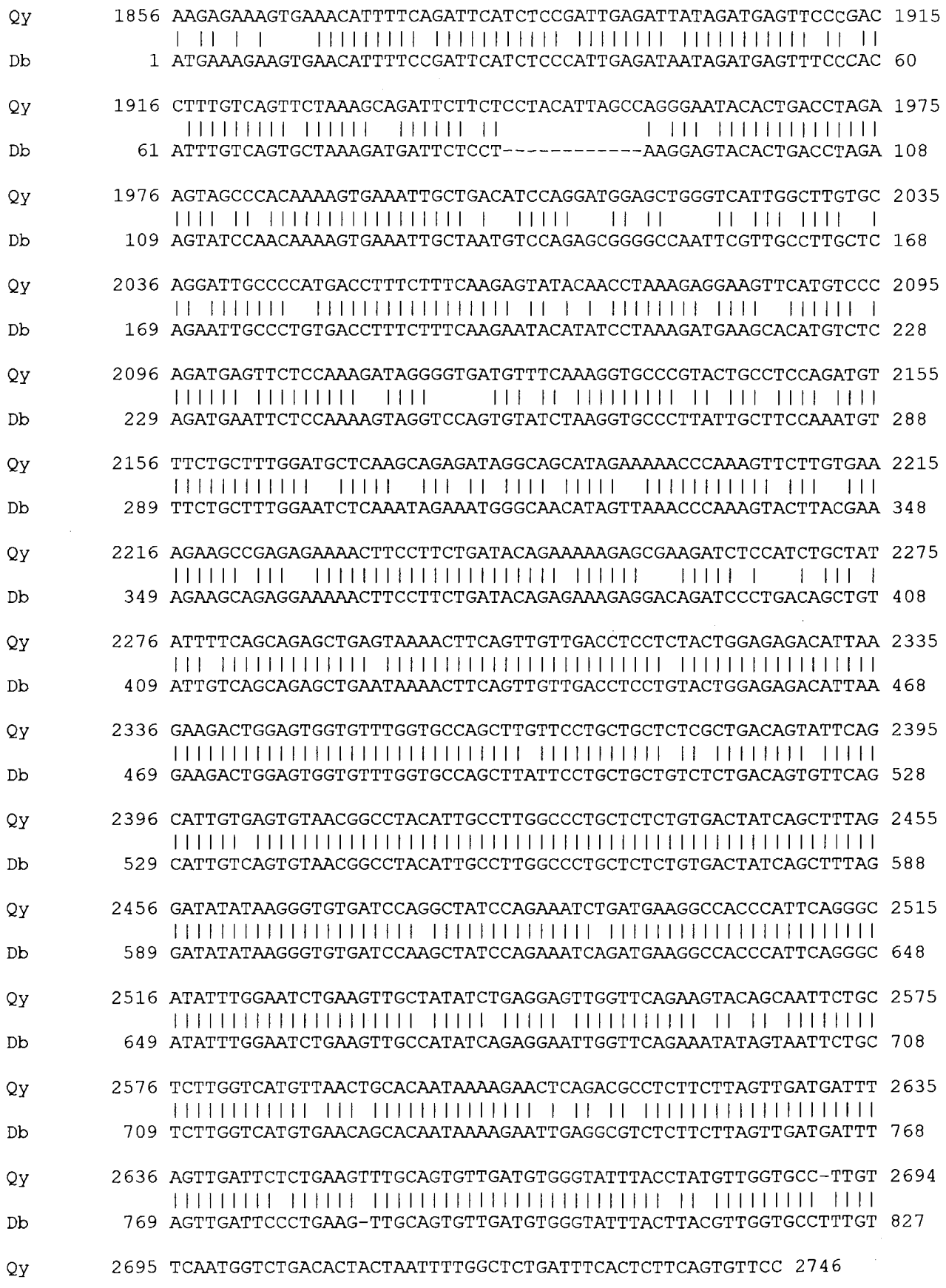

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Db        828 TCAATGGTTTGACACTACTGATTTTAGCCCTGATCTCACTCTTCAGTATTCC 879


RESULT 6
CK231727
LOCUS       CK231727                1003 bp    mRNA    linear   EST 09-DEC-2003
DEFINITION  ILLUMIGEN_MCQ_2869 Katze_MMBR Macaca mulatta cDNA 5' similar to
            human RTN4 (Hs.436349), mRNA sequence.
ACCESSION   CK231727
VERSION     CK231727.1  GI:39638085
KEYWORDS    EST.
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 1003)
  AUTHORS   Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
  TITLE     Large-scale Rhesus Macaque cDNA Sequencing
  JOURNAL   Unpublished (2003)
COMMENT     Contact: C. Magness
            Illumigen Biosciences Inc.
            2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
            Tel: 2063780400
            Fax: 2063780408
            Email: cmagness@illumigen.com
            Sequenced on 2003.11.24. 765 Q20 bases. Assembles in contig w/ 2
            member(s). Contig contains 1 (1.5%) lib members.
            PCR PRimers
            FORWARD: CCCTCACTAAAGGGAACAAAA
            BACKWARD: CACTATAGGGCGAATTGGGTA
            Insert Length: 1003   Std Error: 0.00
            Plate: CL000026  row: D  column: 03
            Seq primer: CCCTCACTAAAGGGAACAAAA
            POLYA=No.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9544"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Katze_MMBR"
                     /note="Organ: brain; Vector: Uni-ZAP XR; Site_1: EcoR I;
                     Site_2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
                     kit (catalog #200400)  and ZAP-CDNA Gigapack III Gold
                     Cloning Kit (Catalog #200450)"
ORIGIN

  Query Match             16.7%;  Score 642;  DB 14;  Length 1003;
  Best Local Similarity   84.1%;  Pred. No. 1e-106;
  Matches  853;  Conservative    0;  Mismatches  125;  Indels   36;  Gaps   10;

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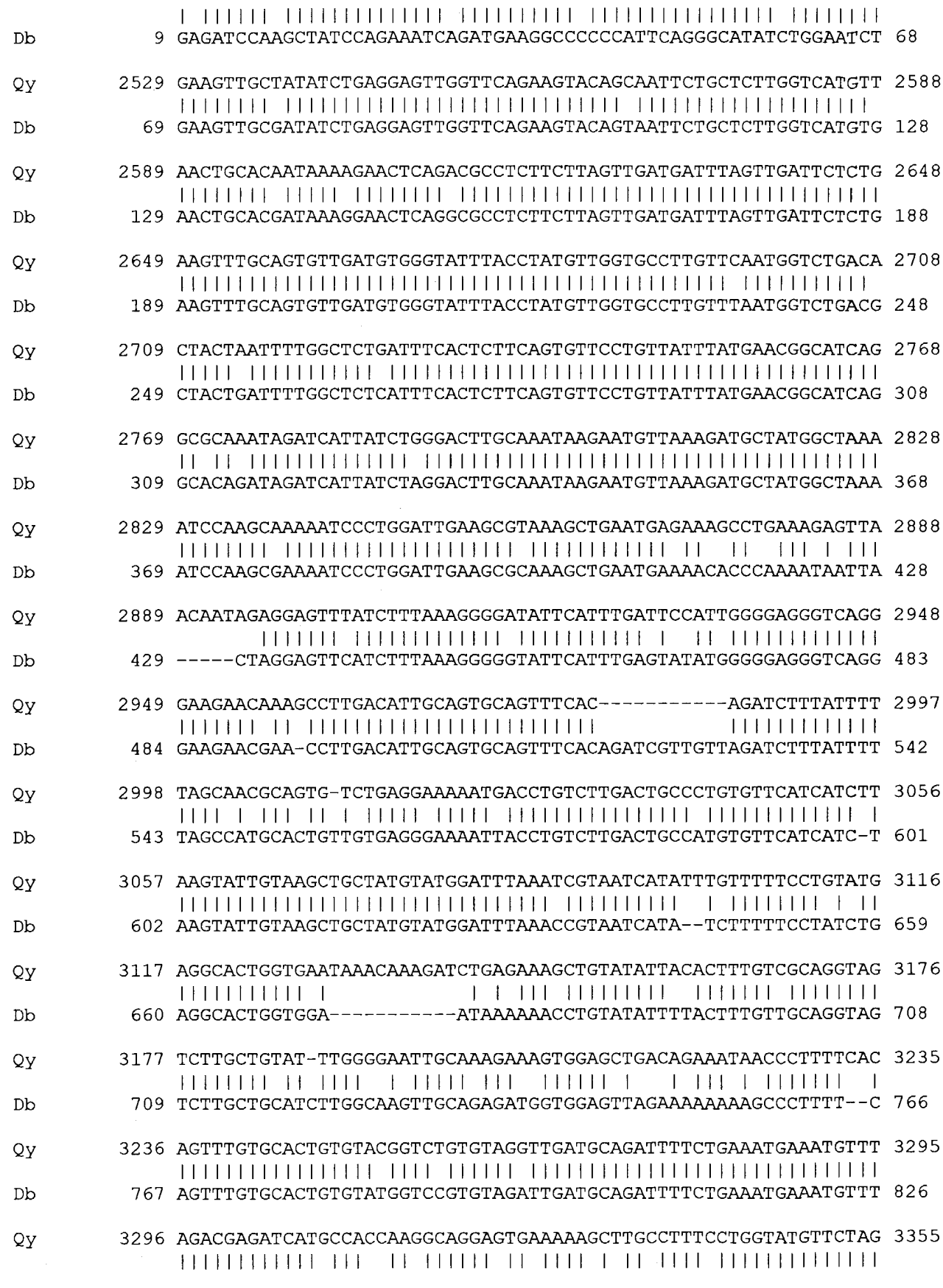

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Db        827 AGACGAGATCATACCAGTAAAGCAGGAATGGAAAATCCTG-CTTTTCTGGTATGTTCTAG 885

Qy       3356 GTGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATAT 3415
              | |||||||||| |||||||| |||||||||| |    |   ||  || |   |||||
Db        886 GGGTATTGTGAATTTTACTGTTATATTAATTGCCCAATATAAGTAAATTATAAATTATAT 945

Qy       3416 ATCTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCAC 3469
              || ||||     |     |        | || |||||||| |||    |||| |
Db        946 ATTTATAGTGGTTTCCCAAAACCTTAAAACCTTTTACCTTTCCAAGCCCCCCCC 999


RESULT 7
CF110956
LOCUS       CF110956                1101 bp    mRNA    linear   EST 23-JUL-2003
DEFINITION  Shultzomica04207 Rat lung airway and parenchyma cDNA libraries
            Rattus norvegicus cDNA clone Contig3732 5', mRNA sequence.
ACCESSION   CF110956
VERSION     CF110956.1  GI:33167337
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V.,
            Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B.,
            Plopper,C.G. and Buckpitt,A.R.
  TITLE     Gene Expression Analysis in Response to Lung Toxicants: I.
            Sequencing and Microarray Development
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Shultz MA
            Dept. of Molecular Biosciences, School of Veterinary Medicine
            University of California, Davis
            1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
            Tel: 530 752 0793
            Fax: 530 752 4698
            Email: mashultz@ucdavis.edu
            Average Phred score is 20 or better. All poor quality data (Phred <
            20) and vector/linker sequence has been removed.
            High quality sequence stop: 1101.
FEATURES             Location/Qualifiers
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                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="Contig3732"
                     /sex="male"
                     /tissue_type="airway or parenchyma"
                     /dev_stage="adult"
                     /clone_lib="Rat lung airway and parenchyma cDNA libraries"
                     /note="Organ: lung; Vector: pGEM-11Zf(-); Site_1: Eco RI;
                     Site_2: Not I; mRNA was isolated from microdissected rat
                     lung airways and parenchyma tissues."
ORIGIN
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Query Match 16.5%; Score 634.2; DB 14; Length 1101;
Best Local Similarity 80.4%; Pred. No. 2.6e-105;
Matches 913; Conservative 0; Mismatches 183; Indels 39; Gaps 13;

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             ||||||||||||| |||||| |||||||||| || |||||||| |||||||||| ||||
Db          1 TGGTGTTTGGTG-CAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTG 59

Qy       2407 TAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGG 2466
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         60 TAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGG 119

Qy       2467 GTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAAT 2526
             | |||||||||||||||||||| |||||||||||||||||||||||||||||| ||||
Db        120 GCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAAT 179

Qy       2527 CTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATG 2586
             |||||||||||||||| ||||| |||||||||| ||||| ||||||||||||||||||
Db        180 CTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATG 239

Qy       2587 TTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTC 2646
             | ||| ||||||||||||||| || || || ||||||||||||||||||||||||||| |
Db        240 TGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCC 299

Qy       2647 TGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGA 2706
             ||||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||
Db        300 TGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGA 359

Qy       2707 CACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATC 2766
             ||||||| ||||| |||||||| |||||||||| ||||||||||||||||||||||||
Db        360 CACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATC 419

Qy       2767 AGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTA 2826
             ||| ||| |||||||||||||| |||||||||| |||| |||||| ||||| ||||| |
Db        420 AGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCA 479

Qy       2827 AAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGT 2886
             |||||||||||||||||||||||||||||| ||||| || ||| ||||||
Db        480 AAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGATTGAAAAAGCC--------- 530

Qy       2887 TAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCA 2946
                | | | || |||| |||||||||||||| | ||| |||||| |    ||| | |  |
Db        531 ---CCAAACAGAAGTTCATCTTTAAAGGGGACACTCACTTGATTAC----GGGGGTGGGA 583

Qy       2947 GGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTTAGCAACGC 3006
             |||           |      | || |||| ||||  ||| ||||||||||||||  ||
Db        584 GGGTCAGGGGTGAGCCCTTGGTGGCCGTGCGGTTT--CAGCTCTTTATTTTTAGCAGTGC 641

Qy       3007 AGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGTA 3066
             | ||| |||||||||| |||||||||||  |||||||| ||||||||||||||||||
Db        642 ACTGTTTGAGGAAAAATTACCTGTCTTGACTT-CCTGTGTTTATCATCTTAAGTATTGTA 700

Qy       3067 AGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGT 3126
             ||||||| ||||||||| |  || ||| ||| | |||| || ||       |   |||||
Db        701 AGCTGCTGTGTATGGATCT-CATTGTAGTCACACTTGTCTTCCCCAATGAGGCGCCTGGT 759

Qy       3127 GAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGTA 3186
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                |||||||  |   || | |||||||||  |||  |  |  |    |||||||| ||||||
Db        760 GAATAAAGGA--CTCGGGGAAAGCTGTGCATTGTATCTGCTGCAGGGTAGTCTAGCTGTA 817

Qy       3187 TTTGGGGAATTGCAAAGAAAGTGGAGCT---GACAGAAATAACCCTTTTCACAGTTTGTG 3243
                |   | || ||| |||||| |   | ||   | |||  | ||||||||||||||  |||
Db        818 TGCAGAGAGTTGTAAAGAAGGCAAATCTGGGGGCAGGGAAAACCCTTTTCACAG--TGTA 875

Qy       3244 CACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGA 3303
                |  ||| |      |||  |  |         |||||||||||||||||||||| ||||
Db        876 CTGTGTTTGGTCAGTGTAAAACTGATGCAGATTTTTCTGAAATGAAATGTTTAGATGAGA 935

Qy       3304 TCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTG 3363
                 ||| | || || ||||    |||||  ||  |  ||  |||| ||||||||||||||||
Db        936 GCATACTACTAAAGCAGAGTGGAAAACTCTGTC--TTTATGGTGTGTTCTAGGTGTATTG 993

Qy       3364 TGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTATAT 3423
                || |||||||||| |    |||||||||||||||||||||||         ||||||||
Db        994 TG-AATTTACTGTTAT----ATTGCCAATATAAGTAAATATAGA----CCTAATCTATAT 1044

Qy       3424 ATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGA 3478
                |||||||||||| ||||||||  |||||  | |  ||||||||||||||||||||
Db       1045 ATAGTGTTTCACAAAGCTTAGATCTTTAACCTTGCAGCTGCCCCACAGTGCTTGA 1099
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RESULT 8
BQ719894
LOCUS       BQ719894                871 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8241298 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6187240 5', mRNA sequence.
ACCESSION   BQ719894
VERSION     BQ719894.1  GI:21858791
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13580  row: o  column: 17
            High quality sequence stop: 677.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6187240"
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/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sympathetic_trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

ORIGIN

Query Match 16.5%; Score 631; DB 13; Length 871;
Best Local Similarity 86.2%; Pred. No. 1e-104;
Matches 731; Conservative 0; Mismatches 110; Indels 7; Gaps 3;

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Qy        909 GAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGTTCAGGAAGCATGT 968
              | ||| |    |||||||||||||||||| || || |||||||| || ||||||||||||
Db         11 GCGGACGCGTGGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAGGAAGCATGT 70

Qy        969 GAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAAATGGACCTG 1028
              |||||||||||||||||| |||||||||||| ||||| | |||||||||||||||| ||
Db         71 GAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAAATGGACTTG 130

Qy       1029 GTTCAAACTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTTTGCCCATCT 1088
              |||||||| ||||||| | |||| |||||||| || |||| | ||||||||||||||||
Db        131 GTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTTTGCCCATCA 190

Qy       1089 TTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATGGAAGCACCA 1148
              |||||||| || |||||||||| ||||| |||||||||||||||| ||||||||||||
Db        191 TTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATGGAAGCACCA 250

Qy       1149 TTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCATCACCATTA 1208
              || ||||||| |||||||||||||||||||||| |   | |||| ||| ||||||||||||
Db        251 TTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCATCACCATTA 310

Qy       1209 GAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAATCCCCCACCA 1268
              ||| |   | |||||||||||||||||||||||   |||||||||||| |||||||||
Db        311 GAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAACCCCCCACCA 367

Qy       1269 TATGAGGAGGCCATGAATGTATCACTAAAAAAAGAATCAGGAATGAATGAAGAAATCACA 1328
              ||||| |||||||||| |||||||||||||||| ||||||||| || |||||||| | |
Db        368 TATGAAGAGGCCATGAGTGTATCACTAAAAAAAGTATCAGGAATAAAGGAAGAAATTAAA 427

Qy       1329 GAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTATATATCTATTGCA 1388
              ||||||||  ||||| || |||| |||| ||||||||||||||||||||||||||||||
Db        428 GAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATTGCA 487

Qy       1389 TGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCTCTAGTTAT 1448
              |||||||||||||||||||||| | ||| |||||||  |||| |||||||||  ||||
Db        488 TGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGATTAT 547
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Qy       1449 TCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTTGAAGATTCC 1508
             |||||||| ||| |||||| |||||||||||| || ||||||||||||||||||||||||
Db        548 TCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTTGAAGATTCC 607

Qy       1509 TCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAGTTCCACAA 1568
             || || ||||||||||||||||||||||||||||||||||||||||| || |||||||||
Db        608 TCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCACAA 667

Qy       1569 AAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCATCTGAGTCA 1628
             |||||||||||| |||| || |||||||||||||  |||||||| | ||||| |||||||
Db        668 AAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGAGTCA 727

Qy       1629 ATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAGGGAGGAAAA 1688
             |||| || | |||| ||||||| |||||||||||||  |   ||||||||||    ||
Db        728 ATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGC---CACCTGAGGGGNAGAAG 784

Qy       1689 CCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAG-CACCTGA 1747
              | || ||||| |||||| ||| |||||||| | ||| | ||||||| | |  ||||||
Db        785 NCATANTTGGAATCTTTTAAGCTCAGTTTAGATAACACNANAGATACCCTGGTTACCTGA 844

Qy       1748 TGAAGTTT 1755
             ||||| ||
Db        845 TGAAGGTT 852
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RESULT 9
CB467517
LOCUS       CB467517                646 bp    mRNA    linear   EST 26-MAR-2003
DEFINITION  733269 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB467517
VERSION     CB467517.1  GI:29273902
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: LAM8011  row: E  column: 7
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
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                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
ORIGIN

  Query Match             16.4%;  Score 628.8;  DB 14;  Length 646;
  Best Local Similarity   99.4%;  Pred. No. 2.9e-104;
  Matches  642;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    1;

Qy       3177 TCTTGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACA 3236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTTGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACA 60

Qy       3237 GTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTA 3296
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Db         61 GTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTA 120

Qy       3297 GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGG 3356
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Db        121 GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGG 180

Qy       3357 TGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGAT--TATATA 3414
             ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        181 TGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATA 240

Qy       3415 TATCTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGC 3474
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        241 TATCTATATATAGTGTTTCATGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGC 300

Qy       3475 TTGATACTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAA 3534
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Db        301 TTGATACTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAA 360

Qy       3535 CGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAAC 3594
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAAC 420

Qy       3595 TCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCTGGA 3654
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCTGGA 480

Qy       3655 CTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT 3714
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT 540

Qy       3715 AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATT 3774
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATT 600

Qy       3775 GTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAA 3820
             |||||||||||||||||||||||||||||||||||| ||||||
Db        601 GTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACCTAAAAA 646
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RESULT 10
BM986175
LOCUS BM986175 627 bp mRNA linear EST 22-MAR-2002
DEFINITION LM24HW00149 Bos taurus LM-24-HW cDNA library Bos taurus cDNA clone LM-24-HW-001-49 (5'), mRNA sequence.
ACCESSION BM986175
VERSION BM986175.1 GI:19684841
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 627)
AUTHORS Yoon,D.H., Jang,Y.S., Kim,T.H., Park,E.W., Lee,H.K., Chung,E.R., Sun,S.S. and Cheong,I.C.
TITLE Gene Expression Profiling of the Bovine skeletal muscle
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Du-Hak Yoon
National Livestock Research Institute, RDA
564 Omockchun-dong, Suwon, 441-350, Korea
Tel: 82 31 290 1593
Fax: 82 31 290 1792
Email: dhyoon@rda.go.kr
Insert Length: 839 Std Error: 0.00
Seq primer: CAGGAAACAGCTATGAC
POLYA=No.
FEATURES Location/Qualifiers
source 1. .627
/organism="Bos taurus"
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/db_xref="taxon:9913"
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/cell_type="myocyte"
/dev_stage="24 months old"
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/clone_lib="Bos taurus LM-24-HW cDNA library"
/note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site_1: EcoRI; Site_2: Xho I"
ORIGIN

Query Match 16.3%; Score 625.4; DB 12; Length 627;
Best Local Similarity 99.8%; Pred. No. 1.2e-103;
Matches 626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2766 CAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCT 2825
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Db          1 CAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCT 60

Qy       2826 AAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAG 2885
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAG 120
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Qy       2886 TTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTC 2945
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTC 180

Qy       2946 AGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTTAGCAACG 3005
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTTAGCAACG 240

Qy       3006 CAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGT 3065
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGT 300

Qy       3066 AAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGG 3125
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Db        301 AAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGG 360

Qy       3126 TGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGT 3185
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Qy       3186 ATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACAGTTTGTGCA 3245
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Qy       3246 CTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATC 3305
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Db        481 CTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATC 540

Qy       3306 ATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTG 3365
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Db        541 ATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTG 600

Qy       3366 AAATTTACTGTTGTATTAATTGCCAAT 3392
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Db        601 AAAATTACTGTTGTATTAATTGCCAAT 627
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RESULT 11
BG570231
LOCUS       BG570231                 843 bp    mRNA    linear   EST 10-APR-2001
DEFINITION  602590632F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717662 5',
            mRNA sequence.
ACCESSION   BG570231
VERSION     BG570231.1  GI:13577884
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 843)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1567 row: o column: 07
High quality sequence stop: 801.

FEATURES Location/Qualifiers
source 1. .843
/organism="Homo sapiens"
/mol_type="mRNA"
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 16.2%; Score 621.4; DB 12; Length 843;
Best Local Similarity 87.6%; Pred. No. 5.9e-103;
Matches 742; Conservative 0; Mismatches 86; Indels 19; Gaps 5;

```
Qy       2304 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 2363
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          2 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 61

Qy       2364 TTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
              | ||||||||||| ||  |||||||||||||||||||||| ||||| ||||||||||||
Db         62 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 121

Qy       2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
             |||||||||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        122 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 181

Qy       2484 CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
             |||||||| ||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        182 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 241

Qy       2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAA 2603
             |||||||||||||||||||||| |||||||||||||||||| |||||||| |||||
Db        242 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 301

Qy       2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 2663
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 361

Qy       2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT 2723
             |||||||||||||||||||||||||||||||| |||||||||||||||| |||||||||
```

```
Db        362 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 421

Qy       2724 CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
              || ||||||||||||||||||||||||||||||||||||||||||| || |||||||||
Db        422 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 481

Qy       2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 541

Qy       2844 CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT 2903
              |||||||||||||| |||||||||||  || |||  ||| | |||       |||||||
Db        542 CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTC 596

Qy       2904 ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTT 2963
              |||||||||||||||| |||||||||  |  ||||||||||  |||||||| || | |
Db        597 ATCTTTAAAGGGGATATCCATTTGATTATACGGGGGAGGGTCCAGGAAGAACGAACCTTG 656

Qy       2964 GACATTGCAGTGCAGTTTCACAGAT----------CTTTATTTTTAGCAACGCAGTG-T 3011
                  ||||||||||||||||||||          ||||||||||||   ||| || | |
Db        657 ACGTTTGCAGTGCAGTTTCACAGATCGTAGTAGATCCTTTATTTTTAGCCCTGCACTGTT 716

Qy       3012 CTGAGGAAAAATGACCTGTCTTGACT-GCCCTGTGTTCATCATCTTAA-GTATTGTAAGC 3069
               ||  | ||||| |||||||||||| ||| |||  |||||||||||| ||||||||||
Db        717 GTGCAGGAAAATTACCTGTCTTGACTGGCCATGTTGTCATCATCTTAAGGTATTGTAAGC 776

Qy       3070 TGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAA 3129
              |||||||||||||||||| ||||       || |  |  ||       | ||||  |||
Db        777 TGCTATGTATGGATTTAAACCGTATCATATCTTTTCCTATCTAATCTGAGGACTGTGGAA 836

Qy       3130 TAAACAA 3136
              | || ||
Db        837 TTAAAAA 843
```

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RESULT 12
CF768055
LOCUS       CF768055                619 bp    mRNA    linear   EST 17-OCT-2003
DEFINITION  CES004952 Bos taurus skin cDNA library Bos taurus cDNA clone
            CCL004952 5', mRNA sequence.
ACCESSION   CF768055
VERSION     CF768055.1  GI:37717274
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 619)
  AUTHORS   Wang,Y.H., McWilliam,S. and Lehnert,S.
  TITLE     Transcription profiling of cattle skin
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Dr Yonghong Wang
            Functional Genomics Lab
            CSIRO Livestock Industries
            Level 5, Queensland Biosciences Precinct, University of Queensland,
            306 Carmody Road St.Lucia QLD Australia
```

Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonghong.Wang@csiro.au
Plate: 6 row: D column: 10.

```
FEATURES             Location/Qualifiers
     source          1. .619
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Hereford Shorthorn"
                     /db_xref="taxon:9913"
                     /clone="CCL004952"
                     /sex="female"
                     /tissue_type="pooled"
                     /dev_stage="Adult"
                     /lab_host="XL1-BlueMRF'strain"
                     /clone_lib="Bos taurus skin cDNA library"
                     /note="Organ: skin; Vector: Uni-ZAPXR; Site_1: EcoRI;
                     Site_2: Xho I; Library made from pooled skin of adult
                     female Hereford-Shorthorn."
ORIGIN
```

Query Match 16.1%; Score 619; DB 14; Length 619;
Best Local Similarity 100.0%; Pred. No. 1.7e-102;
Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2507 ATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAG 2566
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAG 60

Qy       2567 CAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGT 2626
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGT 120

Qy       2627 TGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGG 2686
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGG 180

Qy       2687 TGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCC 2746
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCC 240

Qy       2747 TGTTATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAA 2806
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGTTATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAA 300

Qy       2807 TGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGA 2866
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGA 360

Qy       2867 ATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTT 2926
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTT 420

Qy       2927 GATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCACAG 2986
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCACAG 480
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Qy       2987 ATCTTTATTTTTAGCAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGT 3046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTTTATTTTTAGCAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGT 540

Qy       3047 TCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTT 3106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTT 600

Qy       3107 TTCCTGTATGAGGCACTGG 3125
              ||||||||||||||||||
Db        601 TTCCTGTATGAGGCACTGG 619
```

RESULT 13
CK232009

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LOCUS       CK232009                1164 bp    mRNA    linear   EST 09-DEC-2003
DEFINITION  ILLUMIGEN_MCQ_3196 Katze_MMPL2 Macaca mulatta cDNA 5' similar to
            human RTN4 (Hs.436349), mRNA sequence.
ACCESSION   CK232009
VERSION     CK232009.1  GI:39638367
KEYWORDS    EST.
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 1164)
  AUTHORS   Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
  TITLE     Large-scale Rhesus Macaque cDNA Sequencing
  JOURNAL   Unpublished (2003)
COMMENT     Contact: C. Magness
            Illumigen Biosciences Inc.
            2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
            Tel: 2063780400
            Fax: 2063780408
            Email: cmagness@illumigen.com
            Sequenced on 2003.11.25. 797 Q20 bases. Assembles in contig w/ 2
            member(s). Contig contains 1 (0%) lib members.
            PCR PRimers
            FORWARD: CCCTCACTAAAGGGAACAAAA
            BACKWARD: CACTATAGGGCGAATTGGGTA
            Insert Length: 1164   Std Error: 0.00
            Plate: CL000027  row: F  column: 08
            Seq primer: CCCTCACTAAAGGGAACAAAA
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .1164
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /strain="Indian"
                     /db_xref="taxon:9544"
                     /sex="male"
                     /dev_stage="newborn infant"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Katze_MMPL2"
                     /note="Organ: placenta; Vector: Uni-ZAP XR; Site_1: EcoR
                     I; Site_2: Xho I; Created from Stratagene ZAP-cDNA
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Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III Gold Cloning Kit (Catalog #200450)"

ORIGIN

Query Match 16.1%; Score 618.6; DB 14; Length 1164;
Best Local Similarity 83.9%; Pred. No. 1.7e-102;
Matches 890; Conservative 0; Mismatches 124; Indels 47; Gaps 15;

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Qy       2428 CCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGA 2487
             | | |||    ||||| |||||||||||| | || | |||||||||||| ||||||||||
Db         48 CGCGGCTGCAGGTGACCATCAGCTTTAGGCT-TACAGGGGTGTGATCCAAGCTATCCAGA 106

Qy       2488 AATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGG 2547
             |||| |||||||||||||||||||||||||| |||||||||||||||| ||||||||||
Db        107 AATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCGATATCTGAGG 166

Qy       2548 AGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAAC 2607
             |||||||||||||||||| |||||||||||||||||| |||||||| ||||| ||||
Db        167 AGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAAC 226

Qy       2608 TCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGT 2667
             |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 TCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGT 286

Qy       2668 GGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGA 2727
             |||||||||||||||||||||||||| |||||||||| ||||| |||||||||||  |
Db        287 GGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACGCTACTGATTTTGGCTCTCA 346

Qy       2728 TTTCACTCTTCAGTGTTCCTGTTATTTATGAAC-GGCATCAGGCGCAAATAGATCATTAT 2786
             |||||||||||||||||||||||||||||| |||||||||| || ||||||||||||
Db        347 TTTCACTCTTCAGTGTTCCTGTTATTTATGAACNGGCATCAGGCACAGATAGATCATTAT 406

Qy       2787 CTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCT 2846
             || ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        407 CTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCGAAAATCCCT 466

Qy       2847 GGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATC 2906
             |||||||||| |||||||||||| ||  ||  ||| | |||       ||||||| |||
Db        467 GGATTGAAGCGCAAAGCTGAATGAAAACACCCAAAATAATTA-----CTAGGAGTTCATC 521

Qy       2907 TTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGAC 2966
             |||||||||| |||||||||| |  || |||||||||||||||||| || |||||||
Db        522 TTTAAAGGGGGTATTCATTTGAGTATATGGGGGAGGGTCAGGGAAGAACGAA-CCTTGAC 580

Qy       2967 ATTGCAGTGCAGTTTCAC-----------AGATCTTTATTTTTAGCAACGCAGTG-TCTG 3014
             |||||||||||||||||           |||||||||||||||| | ||| || | ||
Db        581 ATTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTG 640

Qy       3015 AGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGTAAGCTGCTA 3074
             ||| ||||| |||||||||||||||| |||||||||||| ||||||||||||||||||||
Db        641 AGGGAAAATTACCTGTCTTGACTGCCATGTGTTCATCATC-TAAGTATTGTAAGCTGCTA 699

Qy       3075 TGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAAC 3134
             |||||||||||||| |||||||||  | |||||||| | |||||||||||| |
Db        700 TGTATGGATTTAAACCGTAATCATA--TCTTTTTCCTATCTGAGGCACTGGTGGA----- 752

Qy       3135 AAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGTAT-TTGGGG 3193
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                    | | ||| |||||||||  ||||||| |||||||||||||||| || ||||
Db        753 ------ATAAAAAACCTGTATATTTTACTTTGTTGCAGGTAGTCTTGCTGCATCTTGGCA 806

Qy       3194 AATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACAGTTTGTGCACTGTGTAC 3253
              | ||||| |||  |||||| |    | ||| | |||||||  ||||||||||||||||||
Db        807 AGTTGCAGAGATGGTGGAGTTAGAAAAAAAAGCCCTTTT--CAGTTTGTGCACTGTGTAT 864

Qy       3254 GGT-CTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATCATGCCAC 3312
              ||| | |||||| |||||||||||||||||||||||||||||||||| ||||||| ||
Db        865 GGTCCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTAGACAAGATCATACCCA 924

Qy       3313 CAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTA 3372
                |     |     ||||   |  |||| |||||||||||||| |||||| ||  ||||
Db        925 GTAAAGCAGGAATGAAAAATCTTGCTTTTCTGGTATGTTCTAGGGGTATTGGGACTTTTA 984

Qy       3373 CTGTTGTATTAATTGCCAAT-ATAAGTAAATATAGATTATATATATCTATATATAGTGTT 3431
              ||| | |||||||||||||| |||||||||||| ||||     || ||     ||||||
Db        985 CTGGTATATTAATTGCCAATAATAAGTAAATATAAATTA-----ATATAATATAAGTGTT 1039

Qy       3432 TCACGAAGCTT---AGCCCTTTACCTTCCCAGCTGCCCCAC 3469
              || | || |||   | || |||||||| |||||  |||| |
Db       1040 TCCCAAAACTTTAAAACCTTTTACCTTTCCAGCCCCCCCCC 1080
```

RESULT 14
BF044381

LOCUS	BF044381 631 bp mRNA linear EST 10-OCT-2000
DEFINITION	BP250021B10D3 Soares normalized bovine placenta Bos taurus cDNA clone BP250021B10D3 5', mRNA sequence.
ACCESSION	BF044381
VERSION	BF044381.1 GI:10761508
KEYWORDS	EST.
SOURCE	Bos taurus (cow)
ORGANISM	Bos taurus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE	1 (bases 1 to 631)
AUTHORS	Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson,J.H.
TITLE	Bovine ESTs
JOURNAL	Unpublished (2000)
COMMENT	Contact: Lewin, H. A. W. M. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA Tel: 217 333 5998 Fax: 217 244 5617 Email: h-lewin@uiuc.edu Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Cross_match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length. PCR PRimers

```
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Insert Length: 631   Std Error: 0.00
            Plate: BP250021B10  row: D  column: 3
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 631.
FEATURES              Location/Qualifiers
     source           1. .631
                      /organism="Bos taurus"
                      /mol_type="mRNA"
                      /db_xref="taxon:9913"
                      /clone="BP250021B10D3"
                      /sex="female"
                      /lab_host="DH10B"
                      /clone_lib="Soares normalized bovine placenta"
                      /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
                      Site_2: NotI; The cDNA library was contributed by the
                      Soares laboratory and it  was constructed and normalized
                      as described by Bonaldo, M.F.,  Lennon, G. and Soares,
                      M.B. (1996), Genome Research 6(9): 791-806. "
ORIGIN

  Query Match             16.1%;  Score 617;  DB 10;  Length 631;
  Best Local Similarity   99.7%;  Pred. No. 4e-102;
  Matches  629;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       2834 AGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAAT 2893
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAAT 60

Qy       2894 AGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGA 2953
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGA 120

Qy       2954 ACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTTAGCAACGCAGTGTCT 3013
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTTAGCAACGCAGTGTCT 180

Qy       3014 GAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGTAAGCTGCT 3073
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGTAAGCTGCT 240

Qy       3074 ATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAA 3133
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAA 300

Qy       3134 CAAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGTATTTGGGG 3193
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGTATTTGGGG 360

Qy       3194 AATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACAGTTTGTGCACTGTGTAC 3253
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACAGTTTGTGCACTGTGTAC 420

Qy       3254 GGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATCATGCCACC 3313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATCATGCCACC 480
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Qy       3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 3373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 540

Qy       3374 TGTTGTATTAATTGCCAATATAAGTAAATATAGAT--TATATATATCTATATATAGTGTT 3431
              |||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        541 TGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATATCTATATATAGTGTT 600

Qy       3432 TCACGAAGCTTAGCCCTTTACCTTCCCAGCT 3462
              |||||||||||||||||||||||||||||||
Db        601 TCACGAAGCTTAGCCCTTTACCTTCCCAGCT 631


RESULT 15
CB521332
LOCUS       CB521332                 822 bp    mRNA    linear   EST 09-JUL-2003
DEFINITION  UI-M-GH0-cem-h-13-0-UI.r1 NIH_BMAP_GH0 Mus musculus cDNA clone
            IMAGE:6841502 5', mRNA sequence.
ACCESSION   CB521332
VERSION     CB521332.1  GI:29354687
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 822)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
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                     /dev_stage="1, 5, and 15 days newborn"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_GH0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
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primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 16.0%; Score 614.2; DB 14; Length 822;
Best Local Similarity 85.4%; Pred. No. 1.2e-101;
Matches 713; Conservative 0; Mismatches 108; Indels 14; Gaps 2;

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Qy       1945 CTACATTAGCCAGGGAATACACTGACCTAGAAGTAGCCCACAAAAGTGAAATTGCTGACA 2004
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Db         109 TCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGA 168

Qy       2065 GTATACAACCTAAAGAGGAAGTTCATGTCCCAGATGAGTTCTCCAAAGATAGGGGTGATG 2124
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Qy       2125 TTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAG 2184
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Qy       2185 GCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATA 2244
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Qy       2305 TTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCT 2364
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Qy       2365 TGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCCT 2424
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Qy       2545 AGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAG 2604
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Qy       2605 AACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGA 2664
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Db        707 AATTGAGGCGTCTCTTCTTAGTTGATGACTTAGTTGATTCCCTGAAGTTTGCAGTGTTGA 766

Qy       2665 TGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTT 2719
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Job time : 9102.67 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 00:39:35 ; Search time 14422.6 Seconds
(without alignments)
11519.006 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
Sequence: 1 ctatctcctctctcagccgc.....ttaaaaaaaaaaaaaaaaa 3833

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
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6: gb_pat:*
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10: gb_ro:*
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12: gb_sy:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	2716	70.9	4070	9	AY123249	AY123249 Homo sapi
	3	2716	70.9	4102	9	AY123245	AY123245 Homo sapi
	4	2716	70.9	4109	9	AY123248	AY123248 Homo sapi
	5	2716	70.9	4123	9	AY123247	AY123247 Homo sapi
	6	2716	70.9	4160	9	AY123246	AY123246 Homo sapi
	7	2716	70.9	4789	9	AY102279	AY102279 Homo sapi
	8	2687.8	70.1	4822	6	AR220865	AR220865 Sequence
	9	2649.8	69.1	4632	9	AF148537	AF148537 Homo sapi
	10	2379.4	62.1	4053	6	AX195249	AX195249 Sequence
	11	2379.4	62.1	4053	9	AB020693	AB020693 Homo sapi
	12	2379.2	62.1	3491	9	AF333336	AF333336 Homo sapi
	13	2372.6	61.9	4166	9	AB040462	AB040462 Homo sapi
	14	2370.4	61.8	4093	6	BD270070	BD270070 Secreted
	15	2223.6	58.0	3579	6	BD249446	BD249446 Protein s
	16	2223.6	58.0	3579	9	HSA251383	AJ251383 Homo sapi
	17	2220.6	57.9	3576	6	AX766050	AX766050 Sequence
	18	2179.4	56.9	4684	10	RNO242961	AJ242961 Rattus no
	19	2168.8	56.6	3815	10	BC032272	BC032272 Mus muscu
	20	2167.2	56.5	4518	10	BC056373	BC056373 Mus muscu
	21	2154.8	56.2	4063	10	AY102280	AY102280 Mus muscu
	22	2154.8	56.2	4627	10	AY102284	AY102284 Mus muscu
	23	2110.8	55.1	2883	9	AF320999	AF320999 Homo sapi
	24	1876.2	48.9	3821	10	AY114152	AY114152 Mus muscu
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	26	1844.4	48.1	2481	9	AF063601	AF063601 Homo sapi
	27	1777.2	46.4	2386	6	AX099401	AX099401 Sequence
	28	1777.2	46.4	2386	6	BD190738	BD190738 Secreted
	29	1746.4	45.6	2958	10	BC032192	BC032192 Mus muscu
c	30	1698	44.3	39674	9	AC092461	AC092461 Homo sapi
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c	32	1698	44.3	162692	2	AC016171	AC016171 Homo sapi
	33	1518	39.6	1721	4	AY164744	AY164744 Bos tauru

	34	1414.6	36.9	1980	6	BD083733	BD083733 Nucleic a
	35	1414.6	36.9	1980	6	BD097380	BD097380 Nucleic a
	36	1378	36.0	60615	10	AY102286	AY102286 Mus muscu
	37	1378	36.0	166516	2	AC135510	AC135510 Mus muscu
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	39	1378	36.0	212042	10	AL929371	AL929371 Mouse DNA
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	41	1364.2	35.6	238341	2	AC133315	AC133315 Rattus no
	42	1234.2	32.2	1738	10	AB073672	AB073672 Mus muscu
	43	1034.4	27.0	1691	9	AF132048	AF132048 Homo sapi
	44	1033.4	27.0	1700	9	AF177332	AF177332 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS AY123250 4060 bp mRNA linear PRI 23-SEP-2003
DEFINITION Homo sapiens RTN4 isoform G (RTN4) mRNA, complete cds; alternatively spliced.
ACCESSION AY123250
VERSION AY123250.1 GI:26800589
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4060)
AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE 22376540
PUBMED 12488097
REFERENCE 2 (bases 1 to 4060)
AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland
REFERENCE 3 (bases 1 to 4060)
AUTHORS Oertle,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland
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ORIGIN
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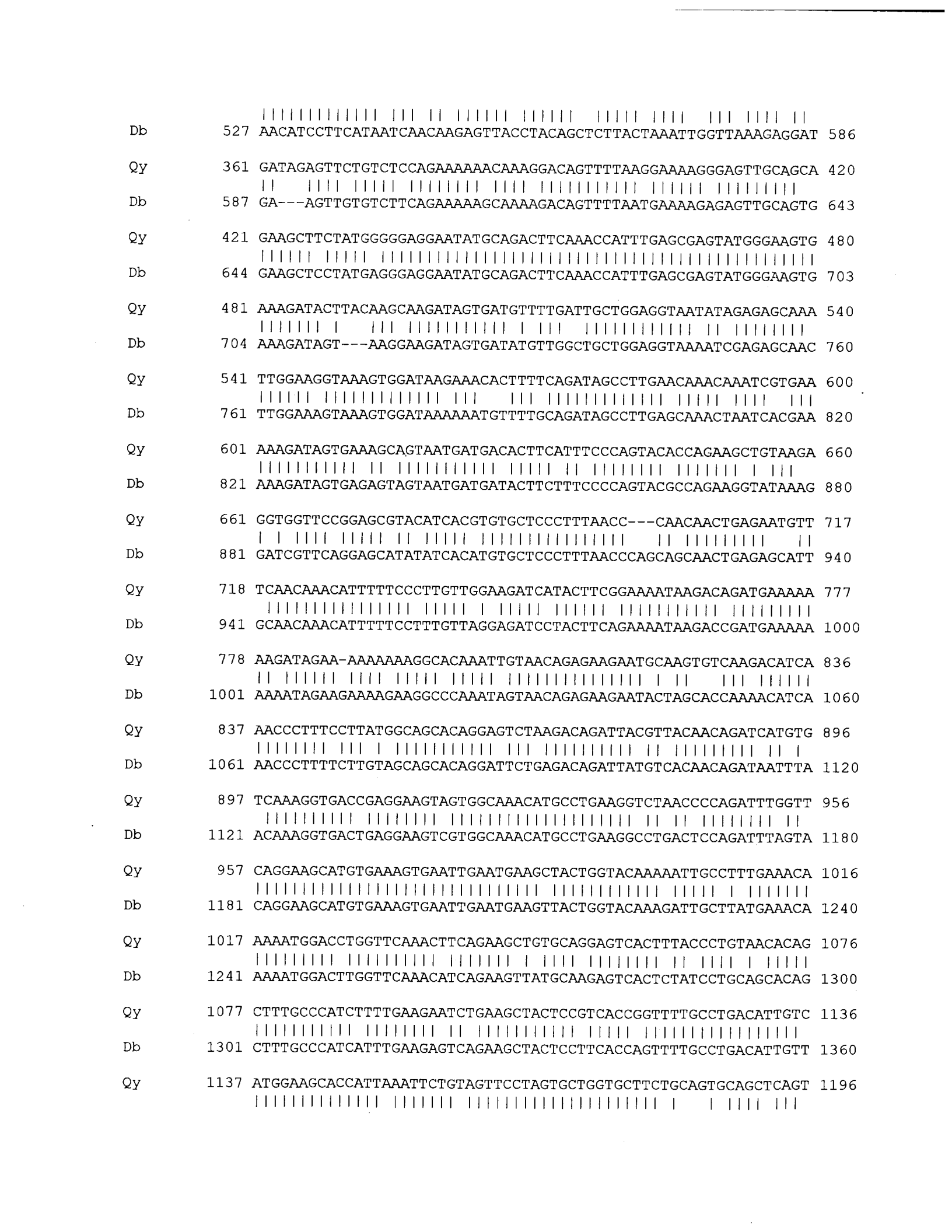

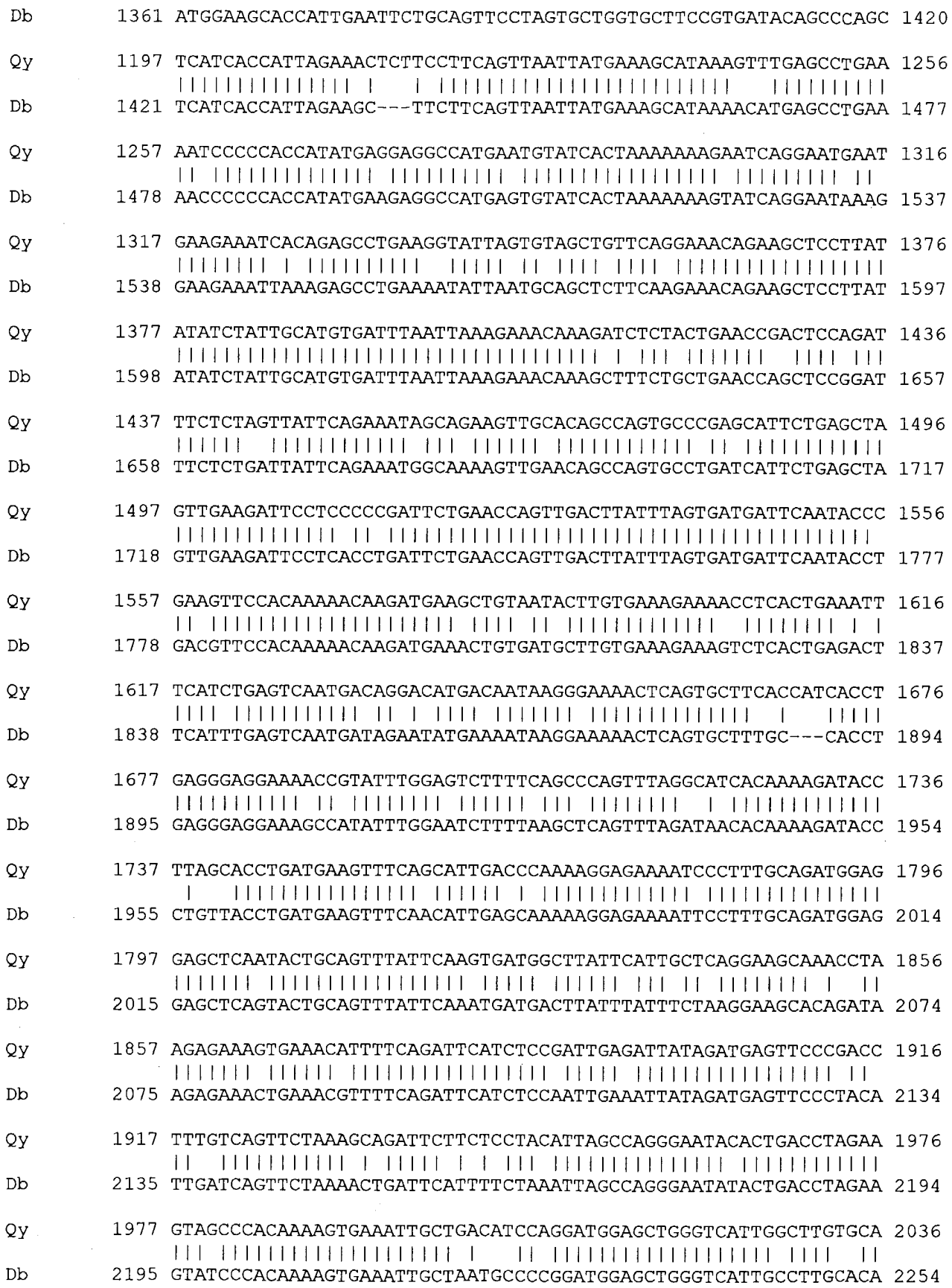

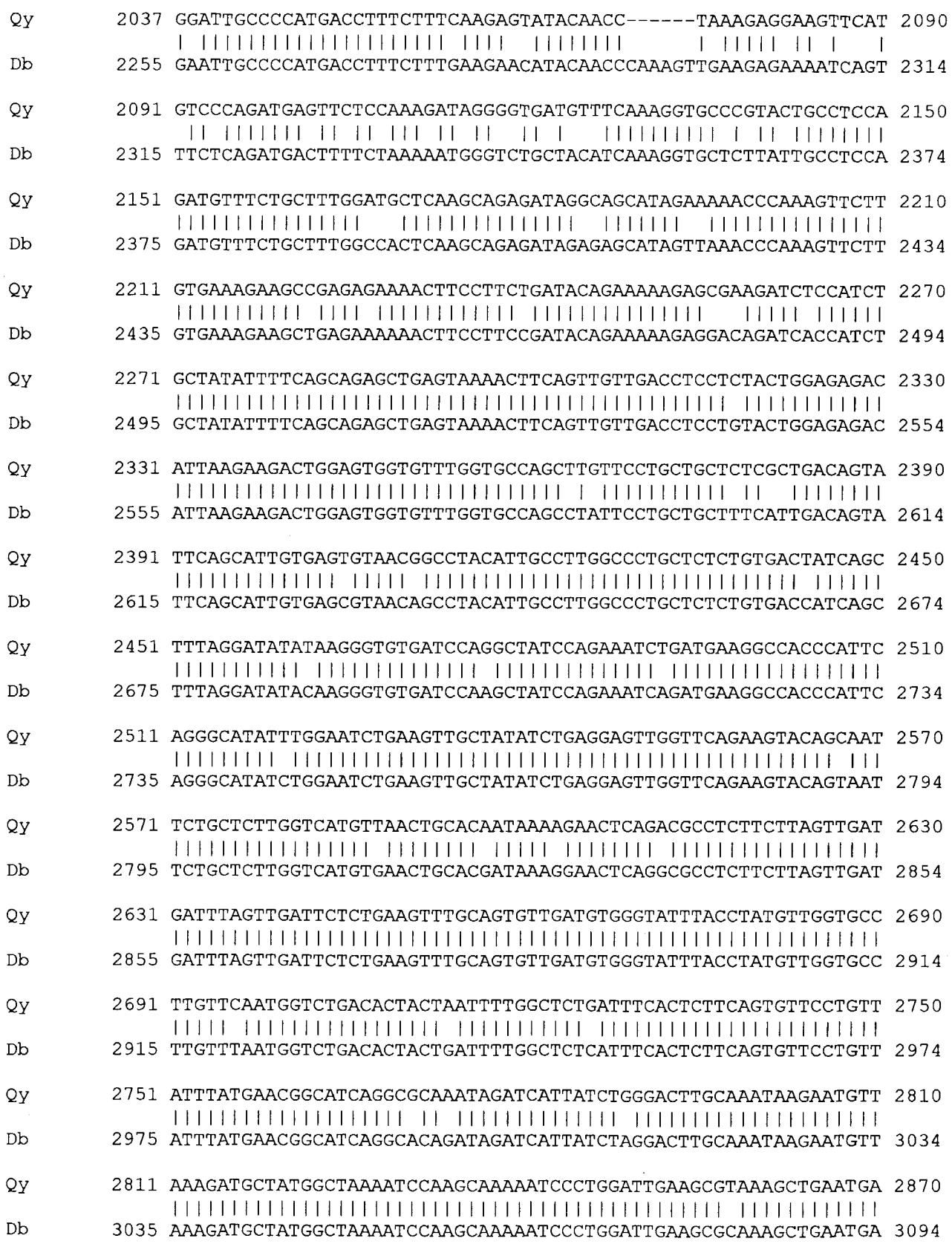

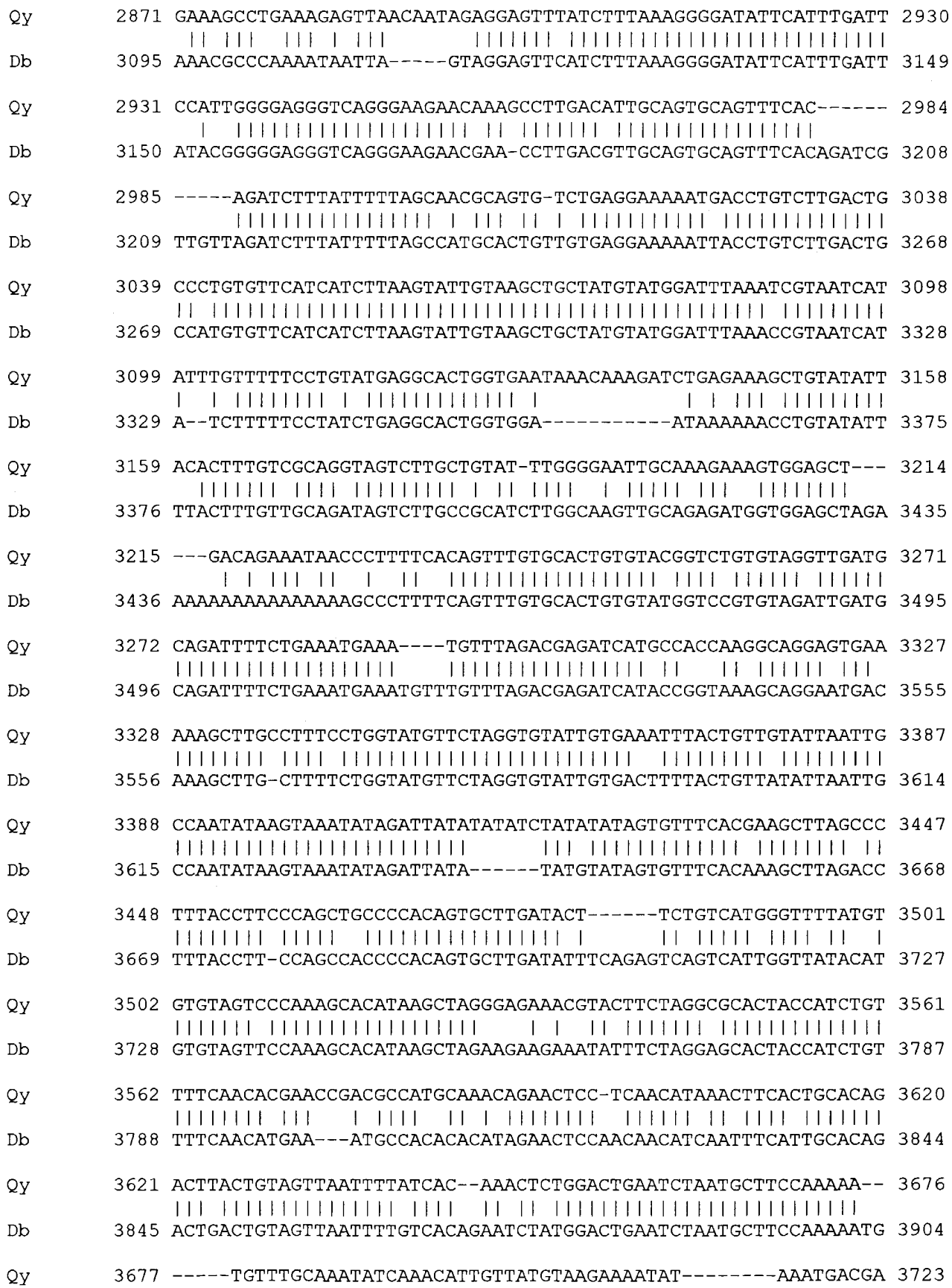

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DEFINITION  Homo sapiens RTN4 isoform F (RTN4) mRNA, complete cds;
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ACCESSION   AY123249
VERSION     AY123249.1  GI:26800586
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4070)
  AUTHORS   Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
  TITLE     Genomic structure and functional characterisation of the promoters
            of human and mouse nogo/rtn4
  JOURNAL   J. Mol. Biol. 325 (2), 299-323 (2003)
  MEDLINE   22376540
   PUBMED   12488097
REFERENCE   2  (bases 1 to 4070)
  AUTHORS   Van der Putten,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
            Inc., Basel, Switzerland
REFERENCE   3  (bases 1 to 4070)
  AUTHORS   Oertle,T. and Schwab,M.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-2002) Brain Research Institute, University of
            Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
            Switzerland
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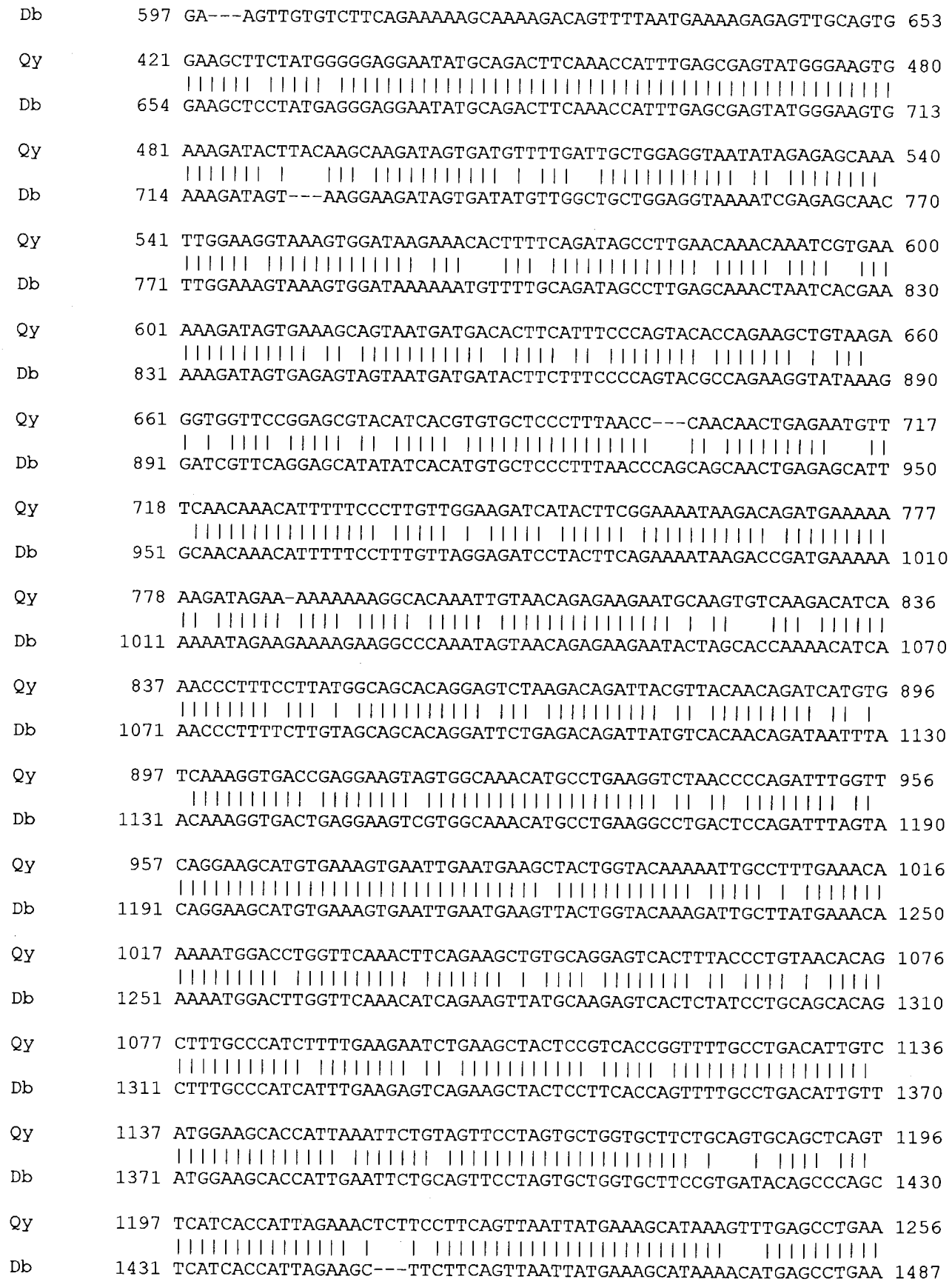

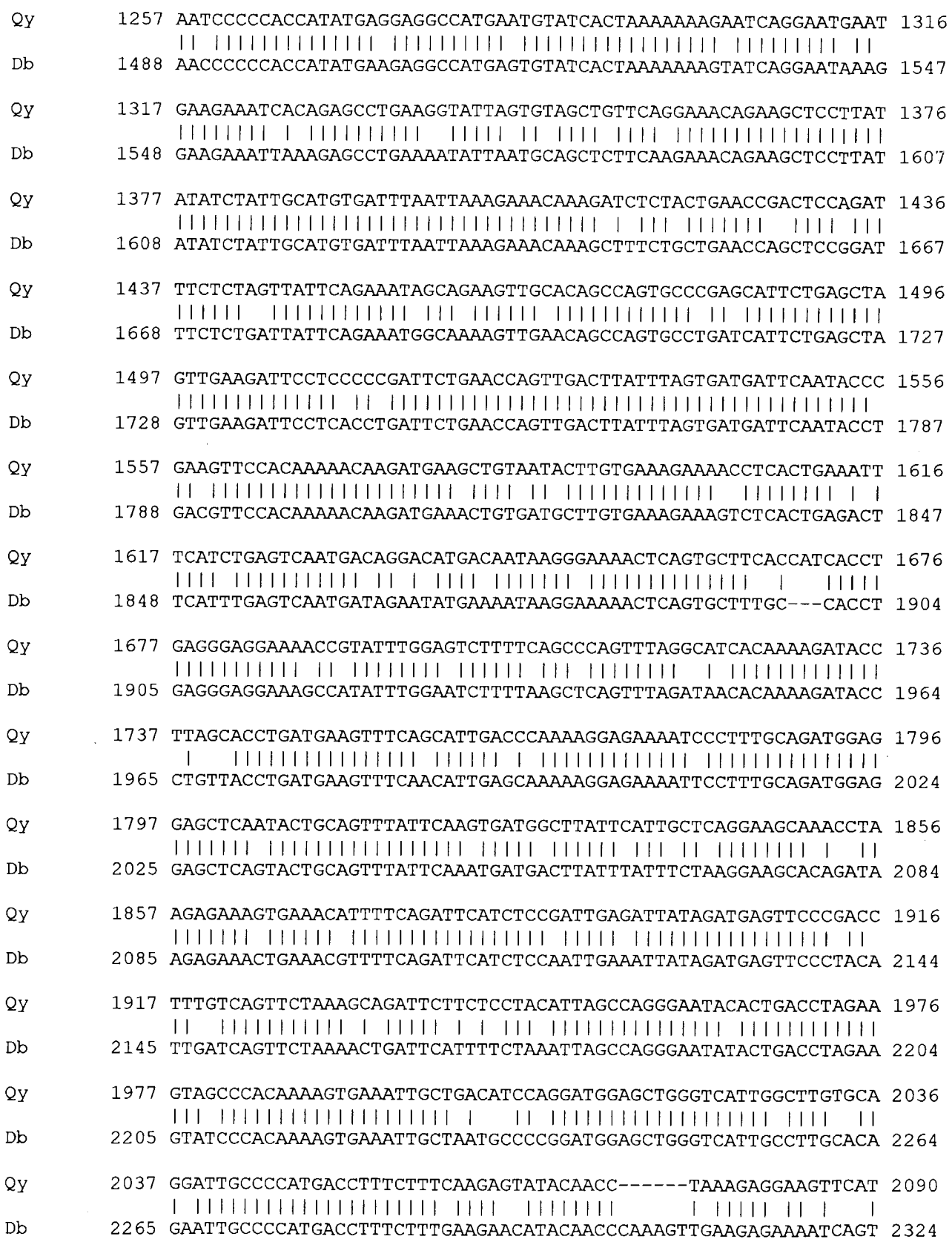

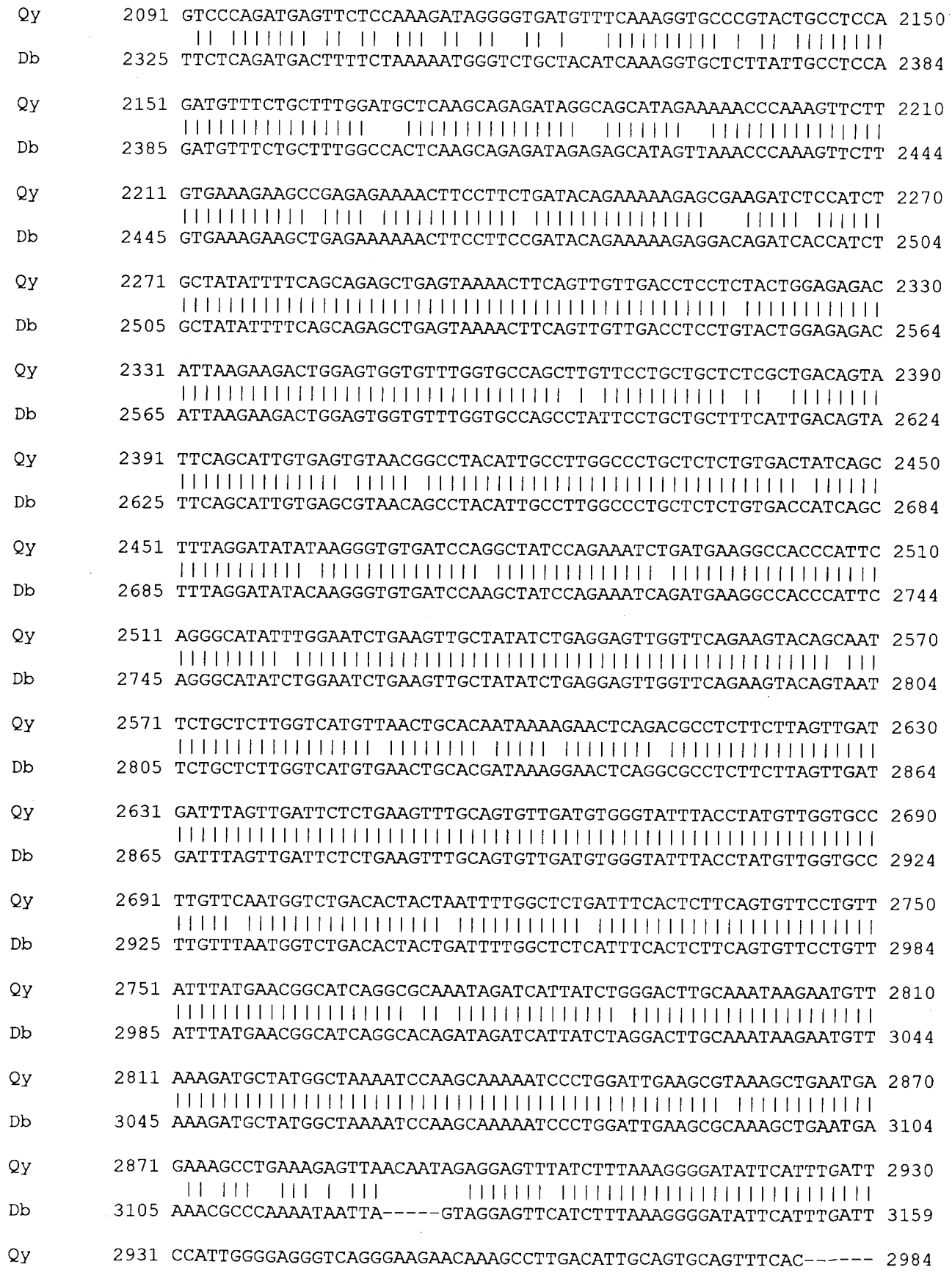

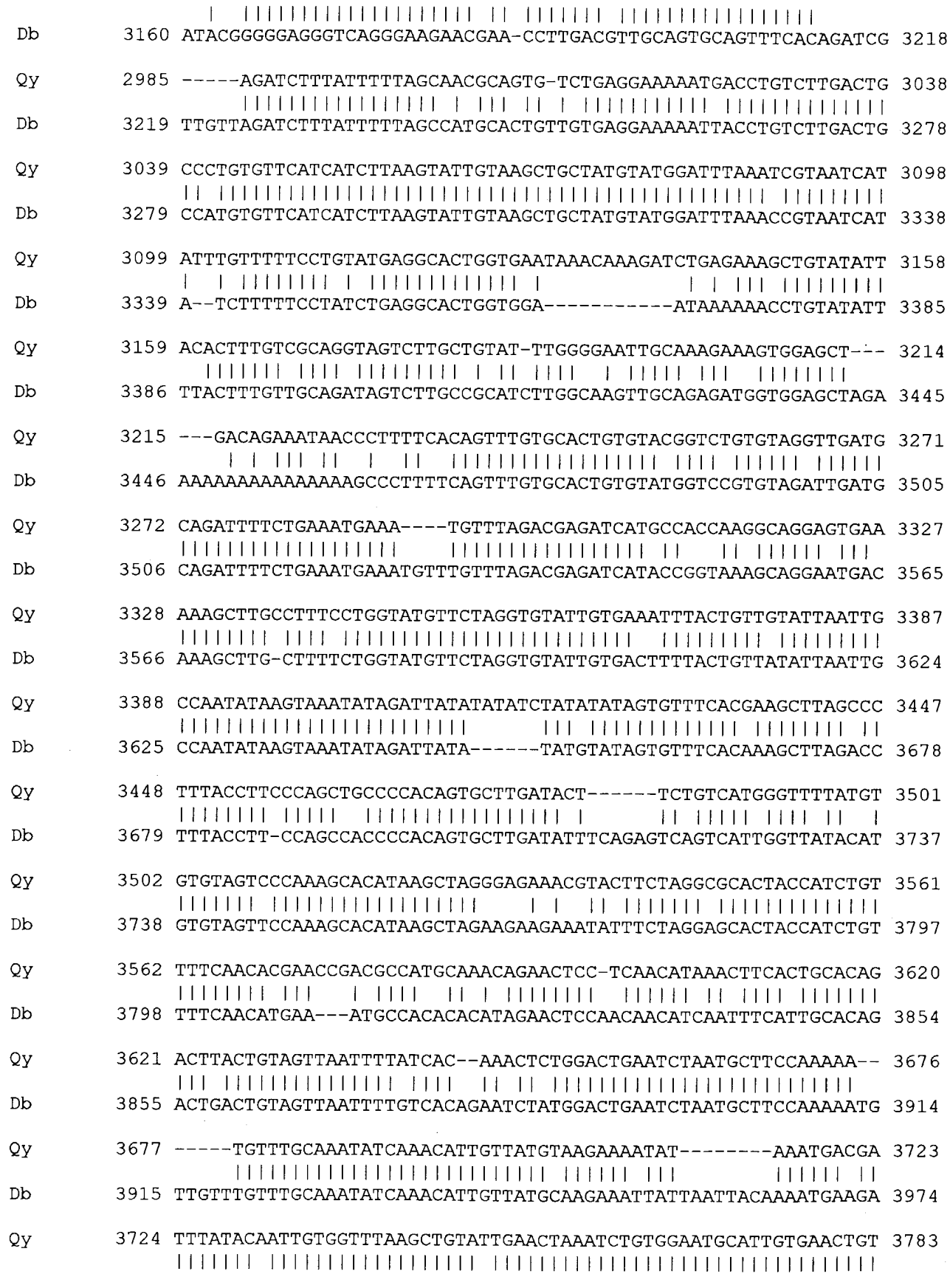

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DEFINITION  Homo sapiens RTN4 isoform Aa (RTN4) mRNA, complete cds;
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ACCESSION   AY123245
VERSION     AY123245.1  GI:26800574
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 4102)
  AUTHORS   Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
  TITLE     Genomic structure and functional characterisation of the promoters
            of human and mouse nogo/rtn4
  JOURNAL   J. Mol. Biol. 325 (2), 299-323 (2003)
  MEDLINE   22376540
   PUBMED   12488097
REFERENCE   2  (bases 1 to 4102)
  AUTHORS   Van der Putten,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
            Inc., Basel, Switzerland
REFERENCE   3  (bases 1 to 4102)
  AUTHORS   Oertle,T. and Schwab,M.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-2002) Brain Research Institute, University of
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ORIGIN

Query Match 70.9%; Score 2716; DB 9; Length 4102;
Best Local Similarity 86.0%; Pred. No. 0;
Matches 3332; Conservative 0; Mismatches 445; Indels 99; Gaps 25;

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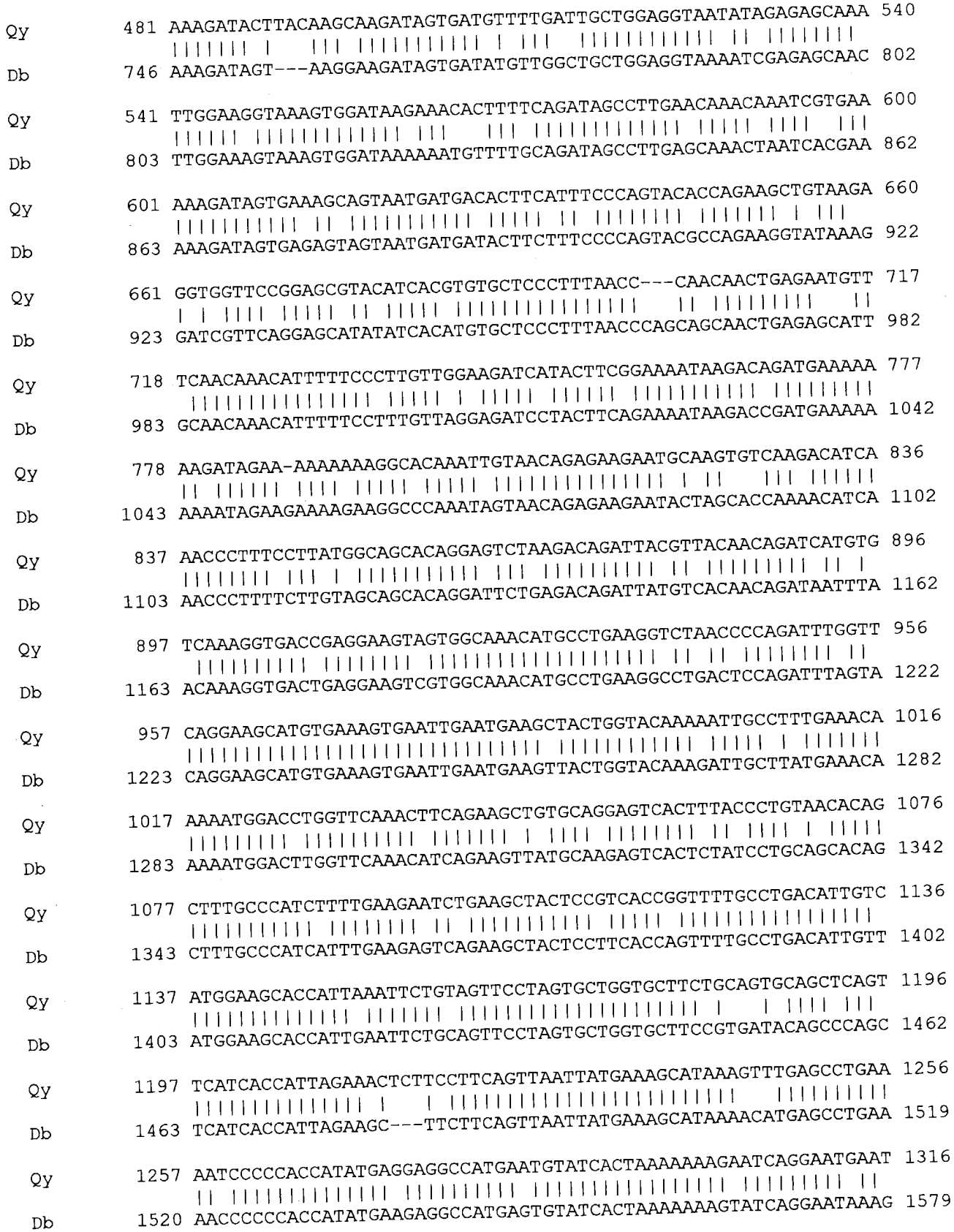

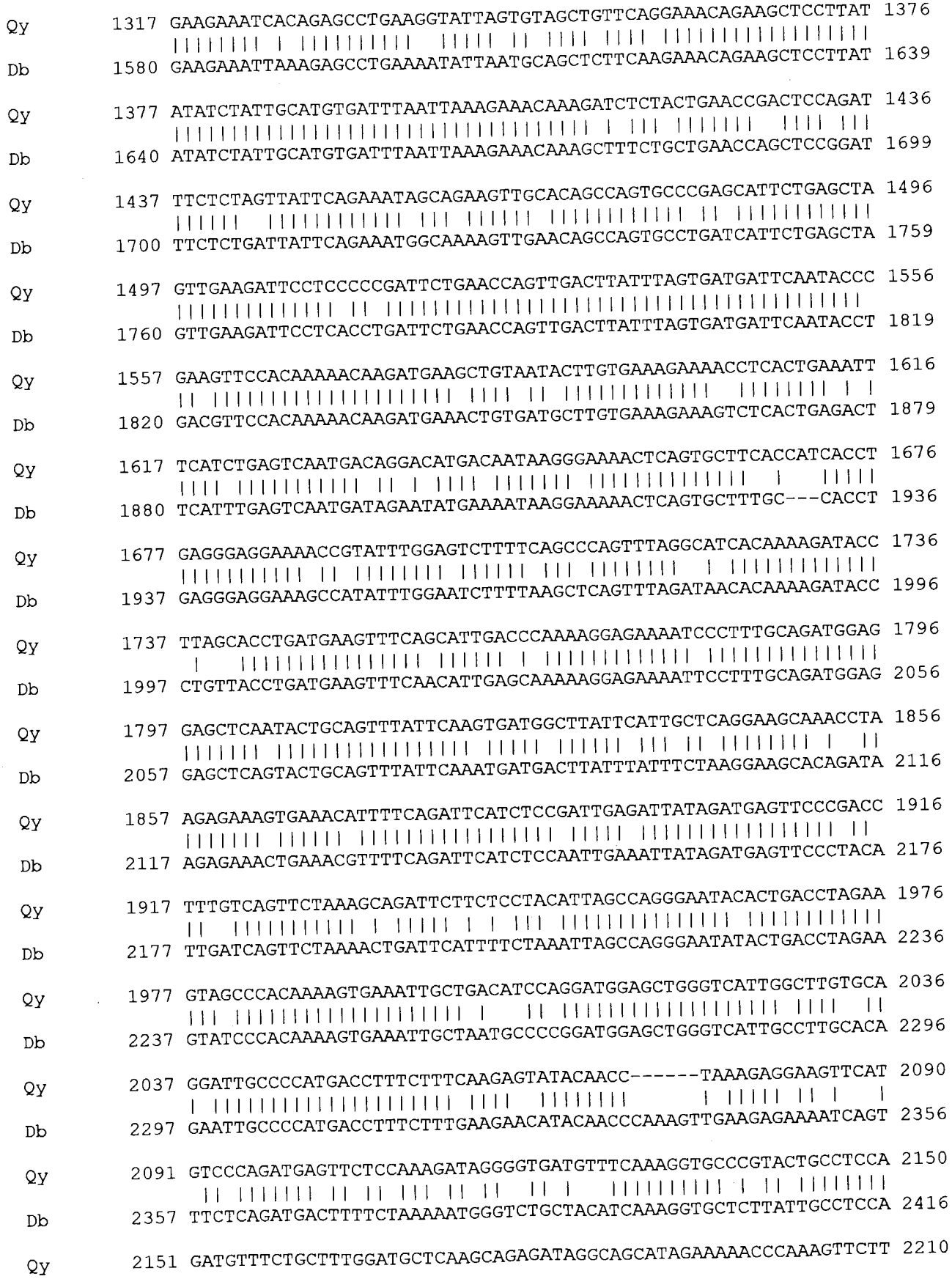

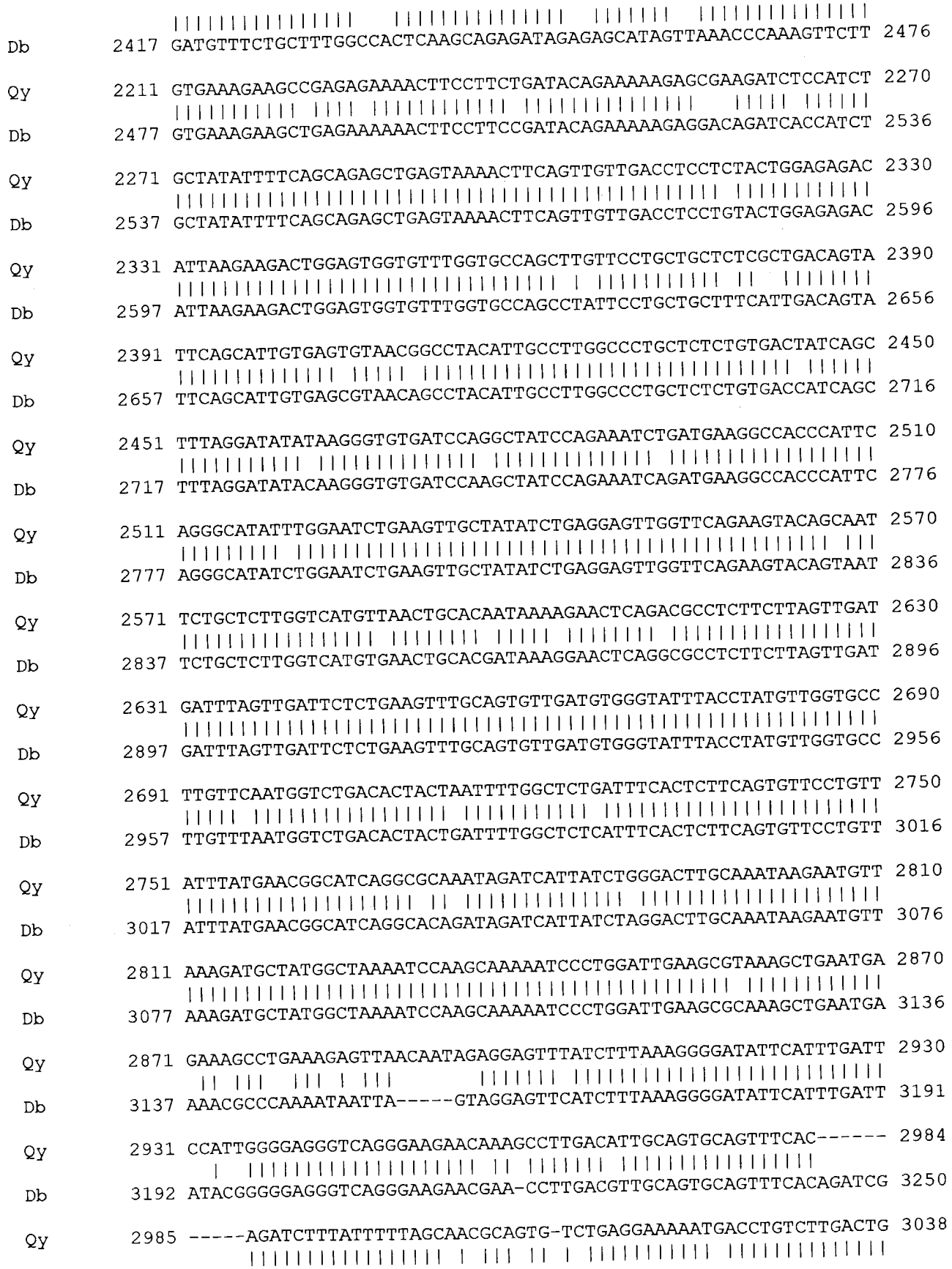

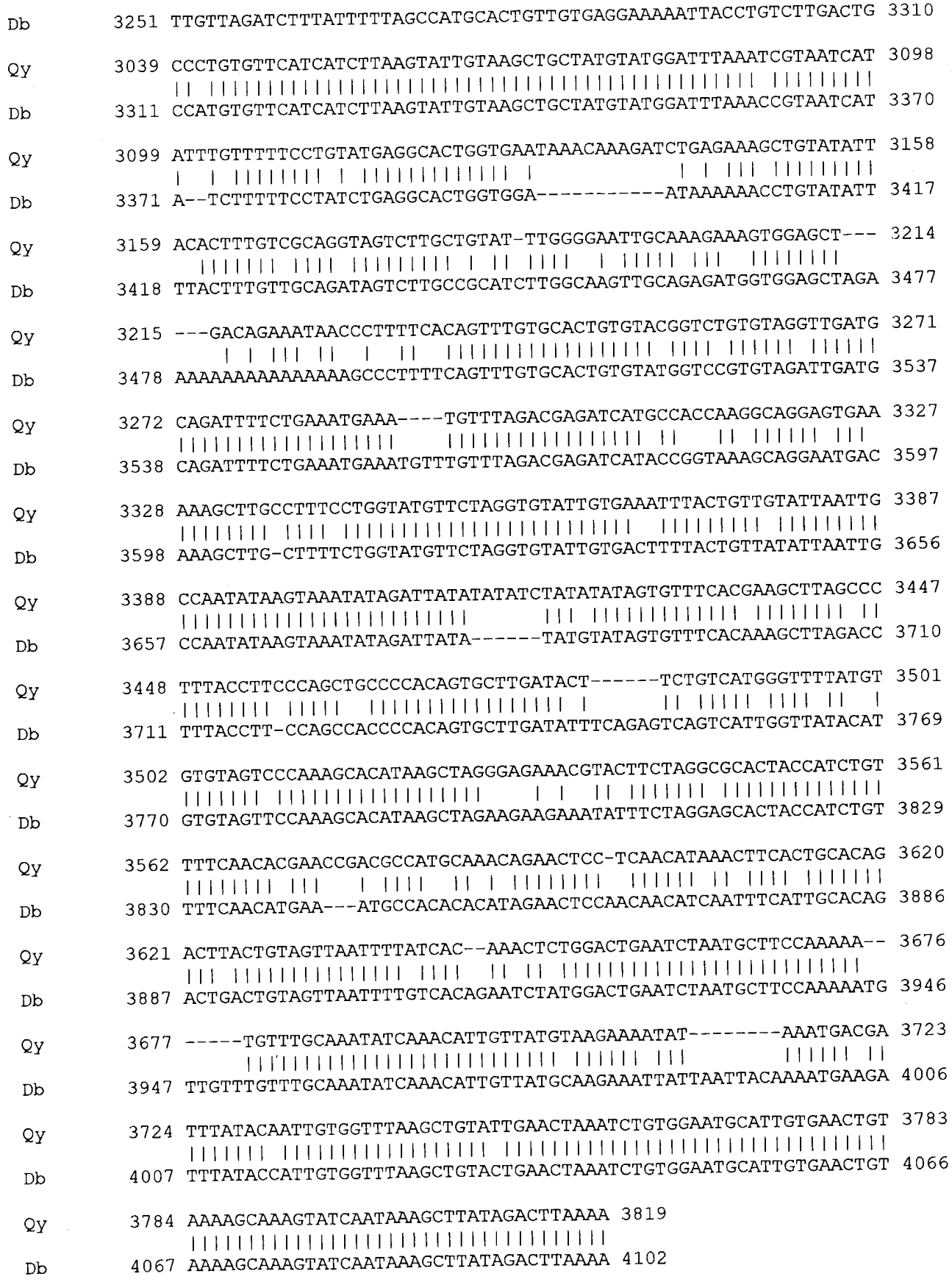

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DEFINITION Homo sapiens RTN4 isoform E (RTN4) mRNA, complete cds; alternatively spliced.
ACCESSION AY123248
VERSION AY123248.1 GI:26800583
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4109)
AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE 22376540
PUBMED 12488097
REFERENCE 2 (bases 1 to 4109)
AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland
REFERENCE 3 (bases 1 to 4109)
AUTHORS Oertle,T. and Schwab,M.E.
TITLE Direct Submission
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ORIGIN

Query Match 70.9%; Score 2716; DB 9; Length 4109;
Best Local Similarity 86.0%; Pred. No. 0;
Matches 3332; Conservative 0; Mismatches 445; Indels 99; Gaps 25;

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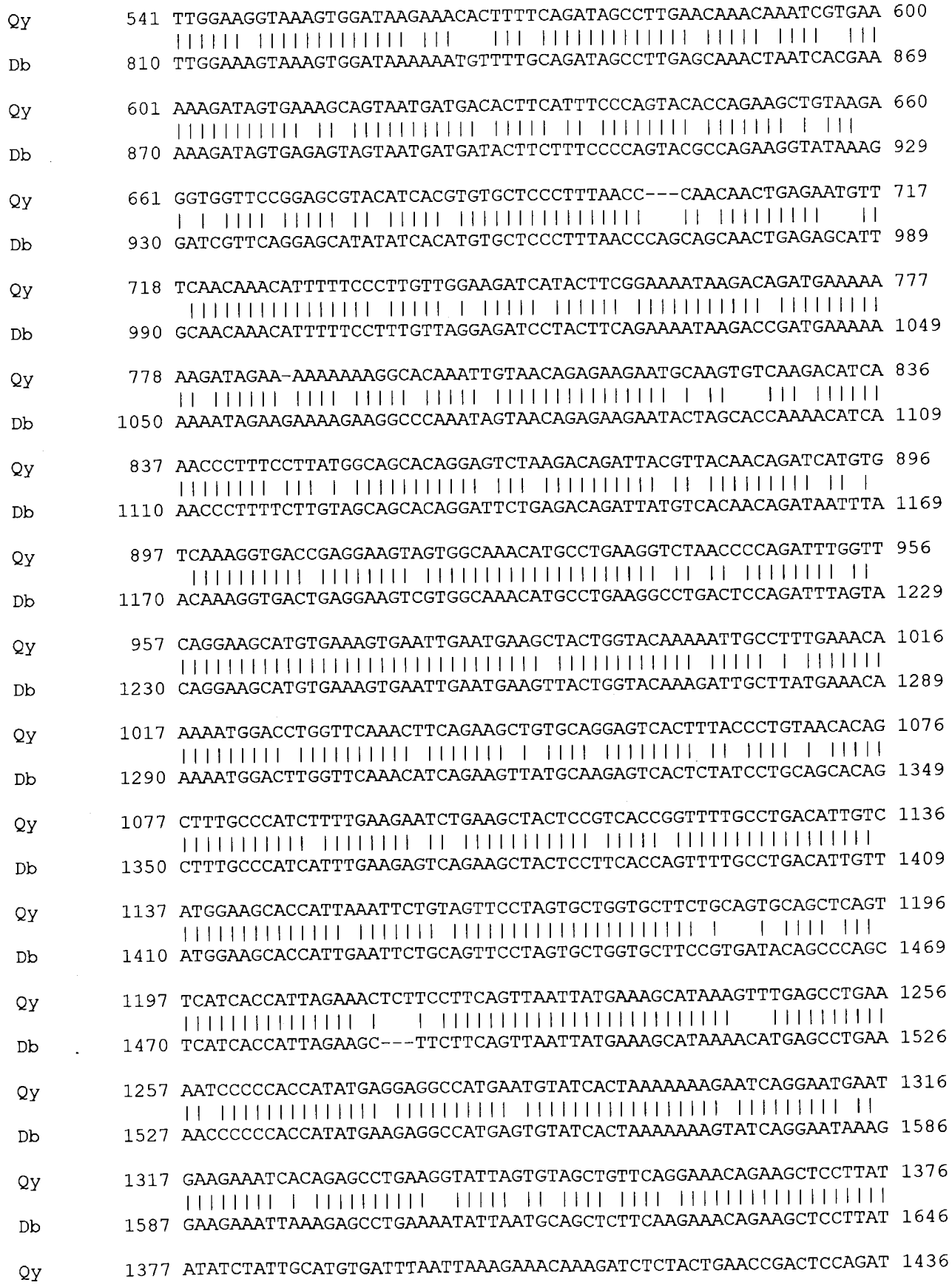

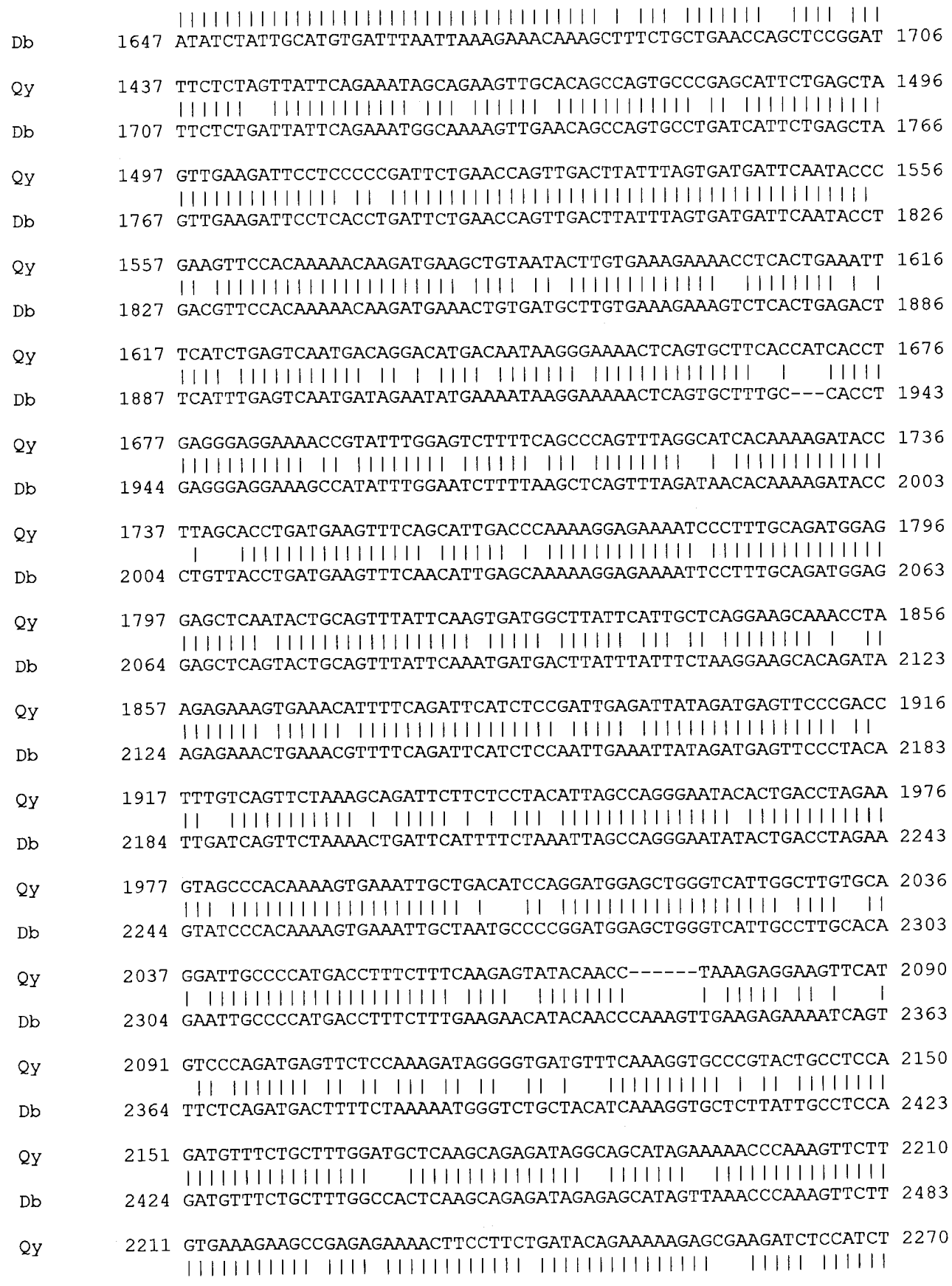

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RESULT 5
AY123247
LOCUS AY123247 4123 bp mRNA linear PRI 23-SEP-2003

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DEFINITION  Homo sapiens RTN4 isoform D (RTN4) mRNA, complete cds;
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ACCESSION   AY123247
VERSION     AY123247.1  GI:26800580
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 4123)
  AUTHORS   Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
  TITLE     Genomic structure and functional characterisation of the promoters
            of human and mouse nogo/rtn4
  JOURNAL   J. Mol. Biol. 325 (2), 299-323 (2003)
  MEDLINE   22376540
   PUBMED   12488097
REFERENCE   2  (bases 1 to 4123)
  AUTHORS   Van der Putten,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
            Inc., Basel, Switzerland
REFERENCE   3  (bases 1 to 4123)
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  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-2002) Brain Research Institute, University of
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ORIGIN

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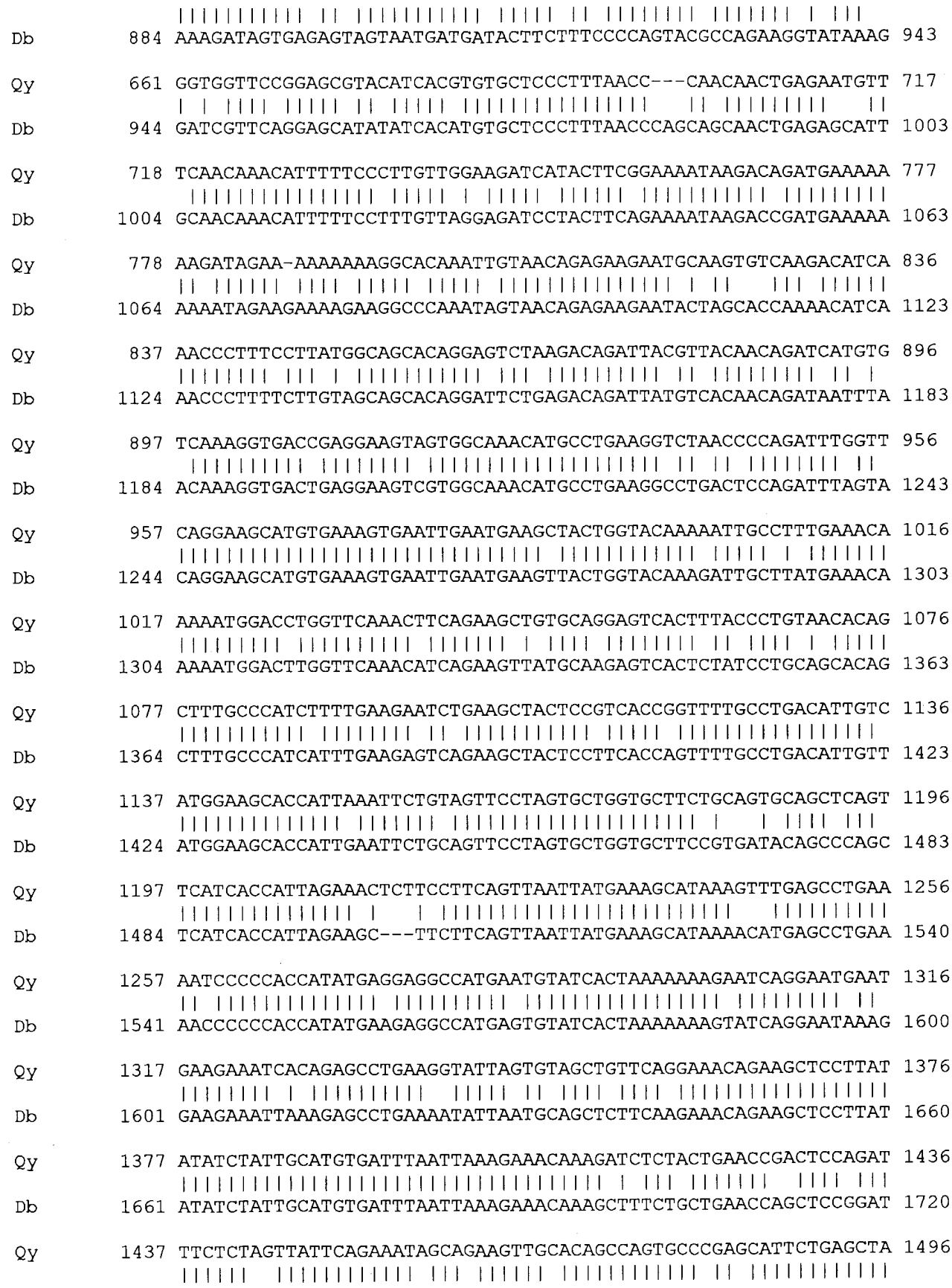

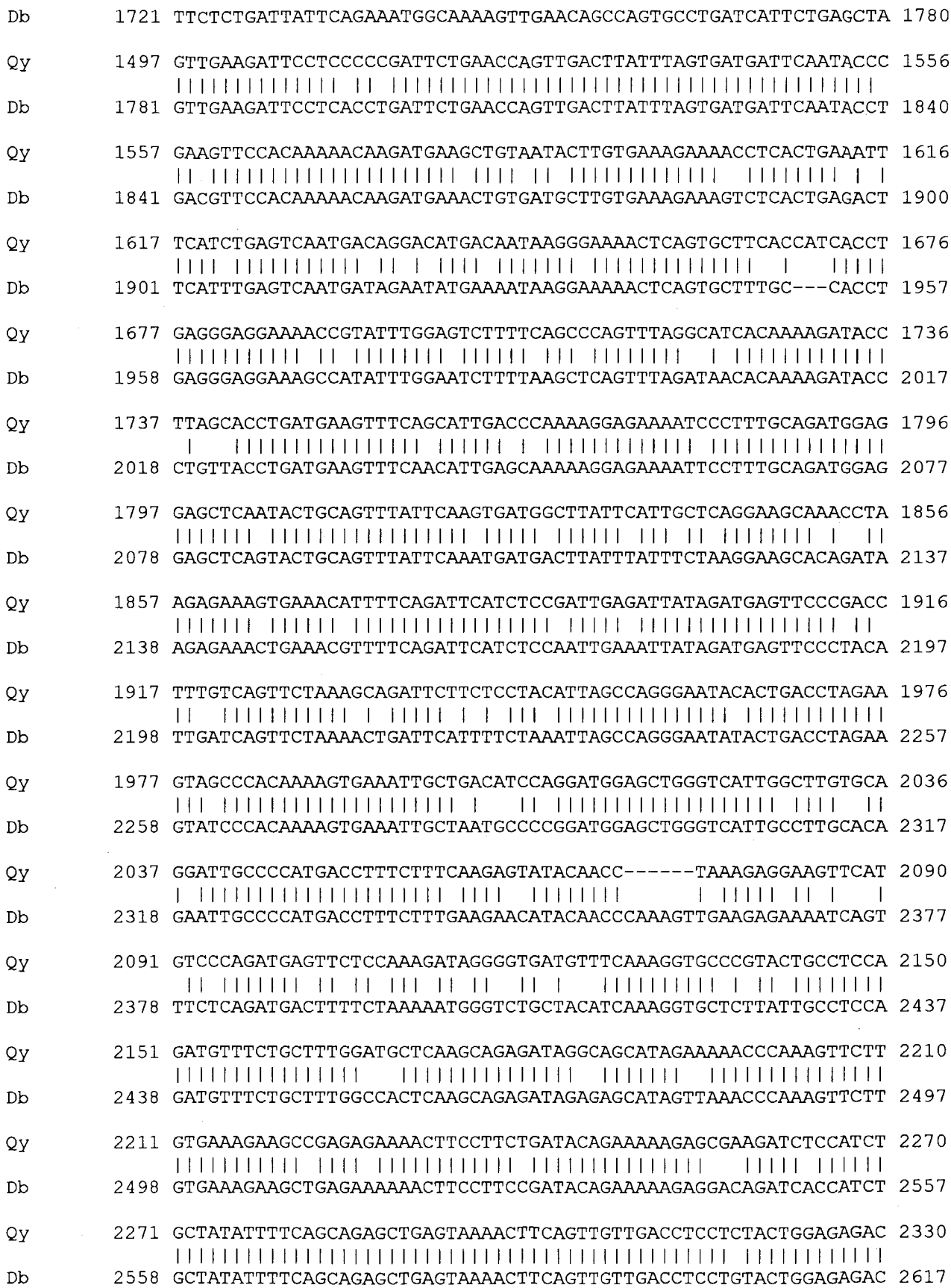

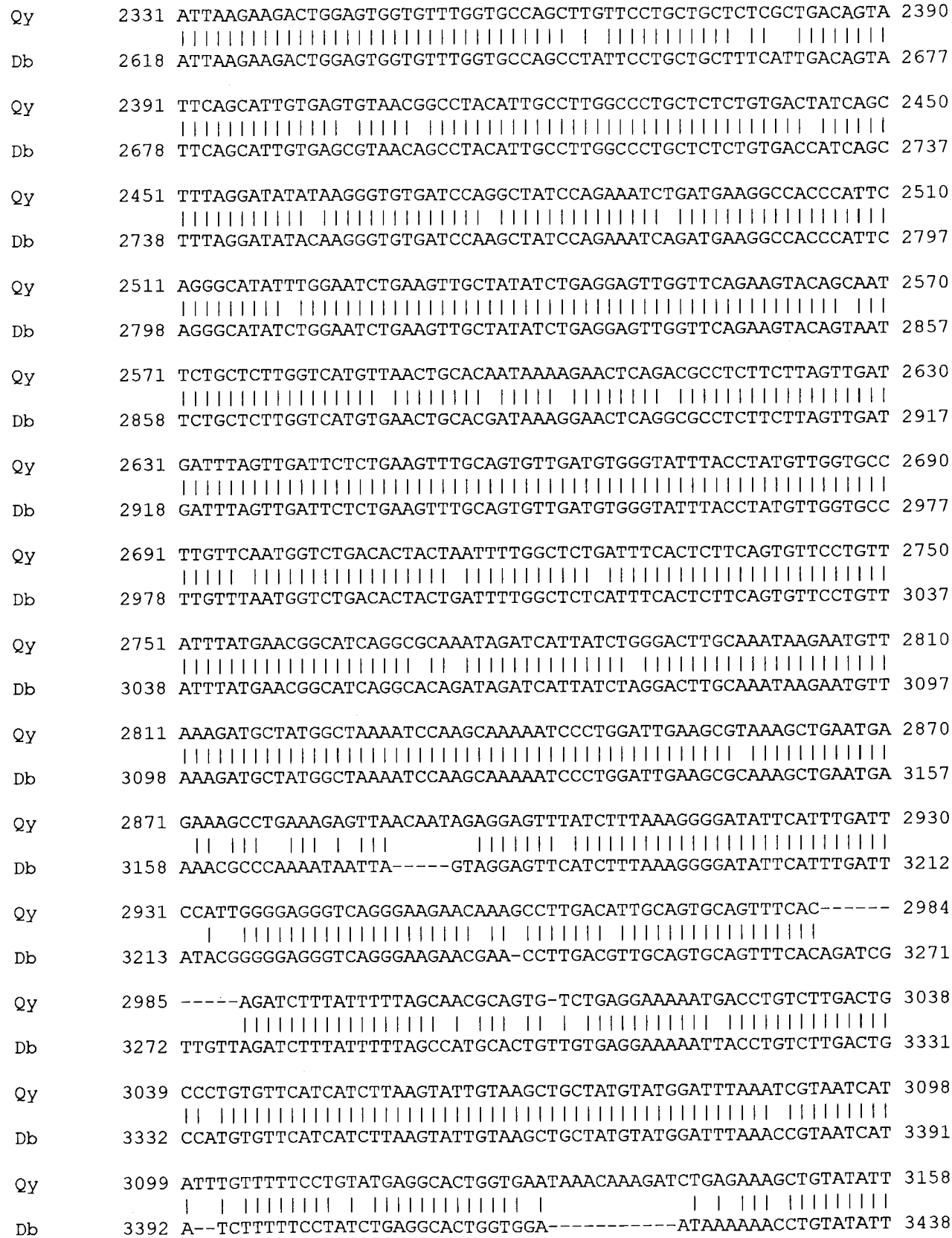

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AY123246
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ACCESSION AY123246
VERSION AY123246.1 GI:26800577
KEYWORDS .

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ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 4160)
AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE 22376540
PUBMED 12488097
REFERENCE 2 (bases 1 to 4160)
AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland
REFERENCE 3 (bases 1 to 4160)
AUTHORS Oertle,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland
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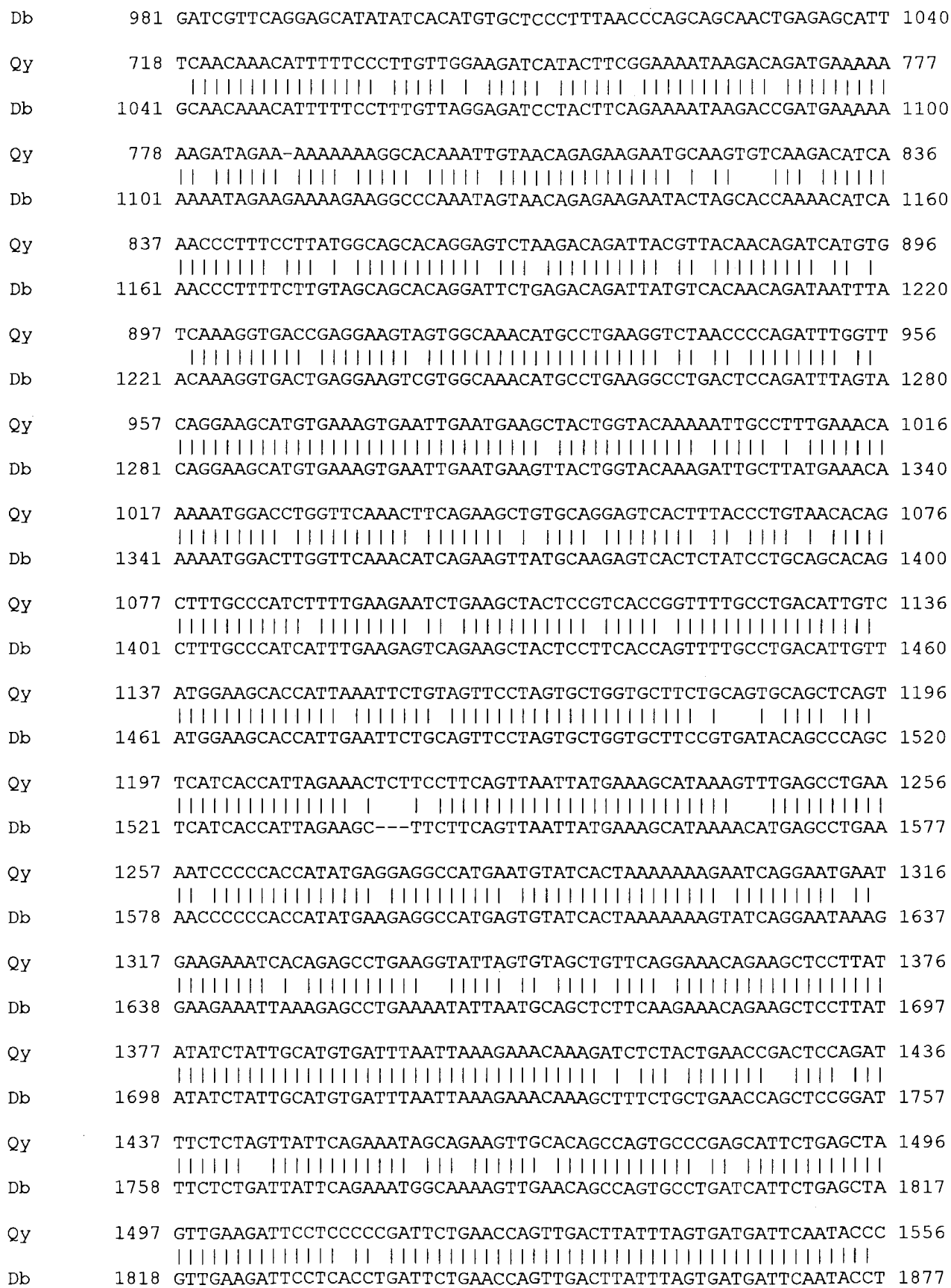

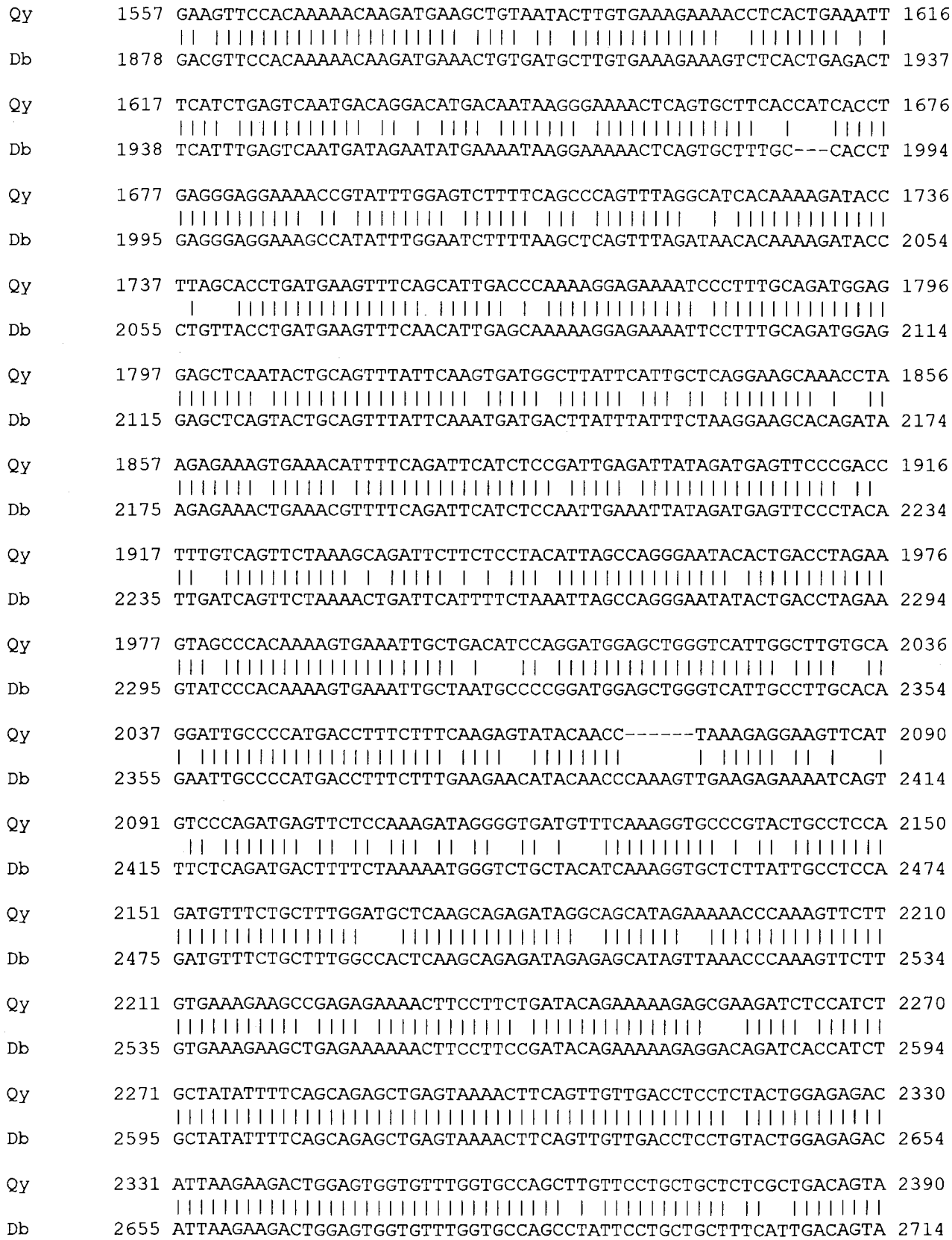

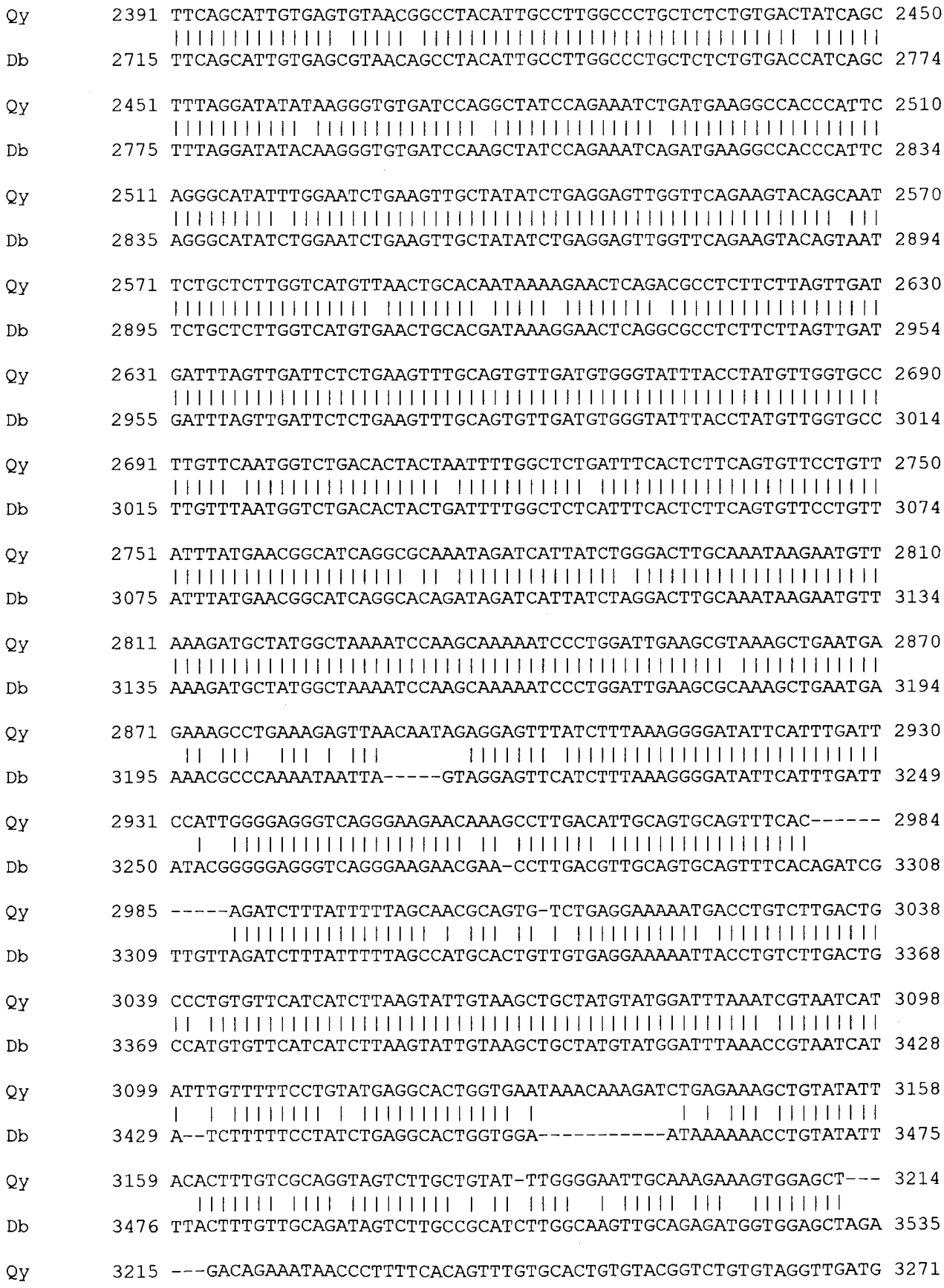

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Qy       3448 TTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT------TCTGTCATGGGTTTTATGT 3501
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Db       3769 TTTACCTT-CCAGCCACCCCACAGTGCTTGATATTTCAGAGTCAGTCATTGGTTATACAT 3827

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Db       3945 ACTGACTGTAGTTAATTTTGTCACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATG 4004

Qy       3677 -----TGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT--------AAATGACGA 3723
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Qy       3724 TTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAACTGT 3783
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Db       4065 TTTATACCATTGTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGT 4124

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AY102279
LOCUS       AY102279                4789 bp    mRNA    linear   PRI 23-SEP-2003
DEFINITION  Homo sapiens RTN4 isoform A (RTN4) mRNA, complete cds;
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ACCESSION   AY102279
VERSION     AY102279.1  GI:26800572
KEYWORDS    .
SOURCE      Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4789)
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AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE 22376540
PUBMED 12488097
REFERENCE 2 (bases 1 to 4789)
AUTHORS Oertle,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland
REFERENCE 3 (bases 1 to 4789)
AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland
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3'UTR 3824. .4789

/gene="RTN4"

ORIGIN

Query Match 70.9%; Score 2716; DB 9; Length 4789;
Best Local Similarity 86.0%; Pred. No. 0;
Matches 3332; Conservative 0; Mismatches 445; Indels 99; Gaps 25;

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Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
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Qy        301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
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Qy        361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
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Qy        481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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Qy        541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
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Qy        601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
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Db       1550 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG 1609

Qy        661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGTT 717
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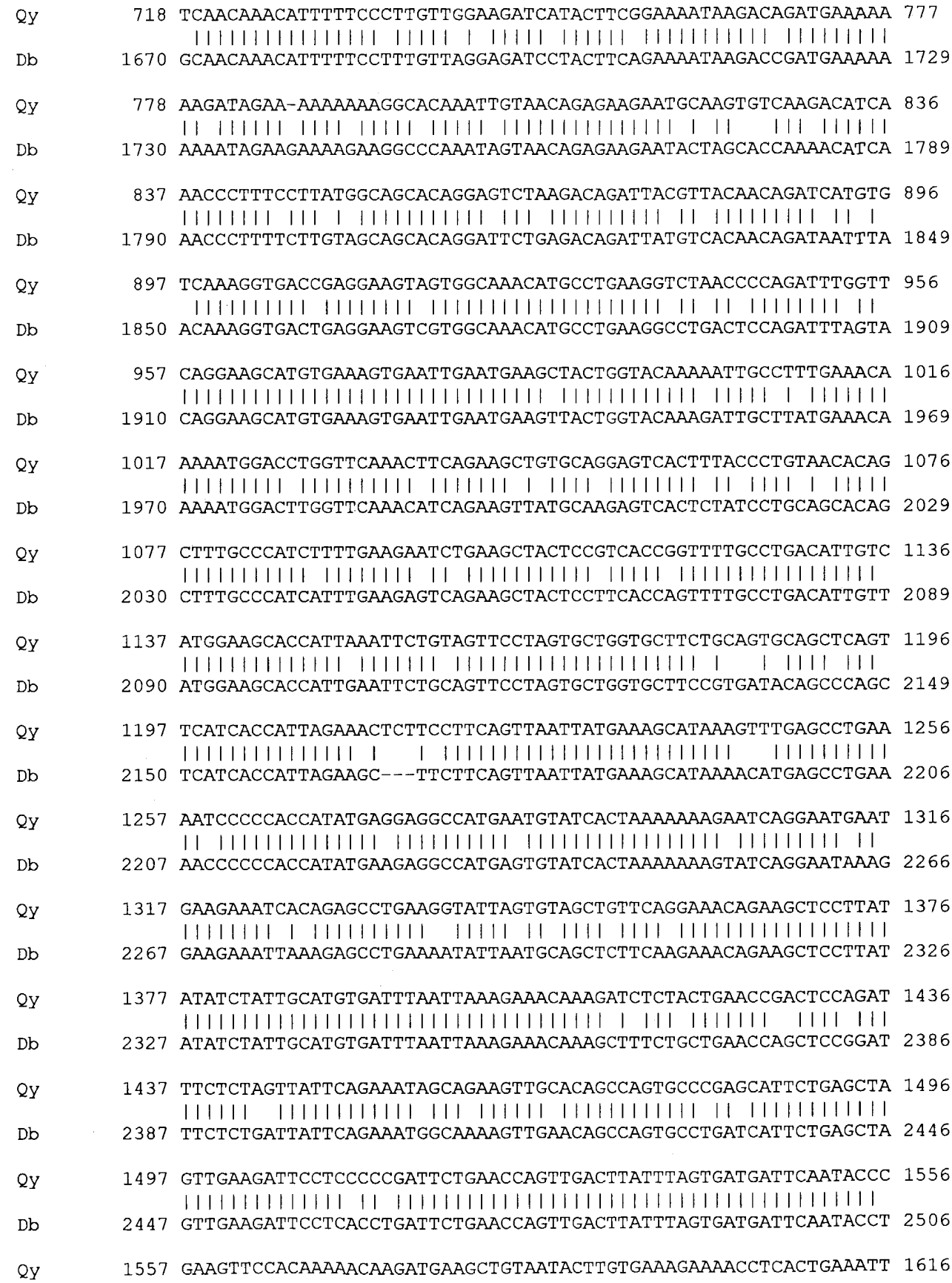

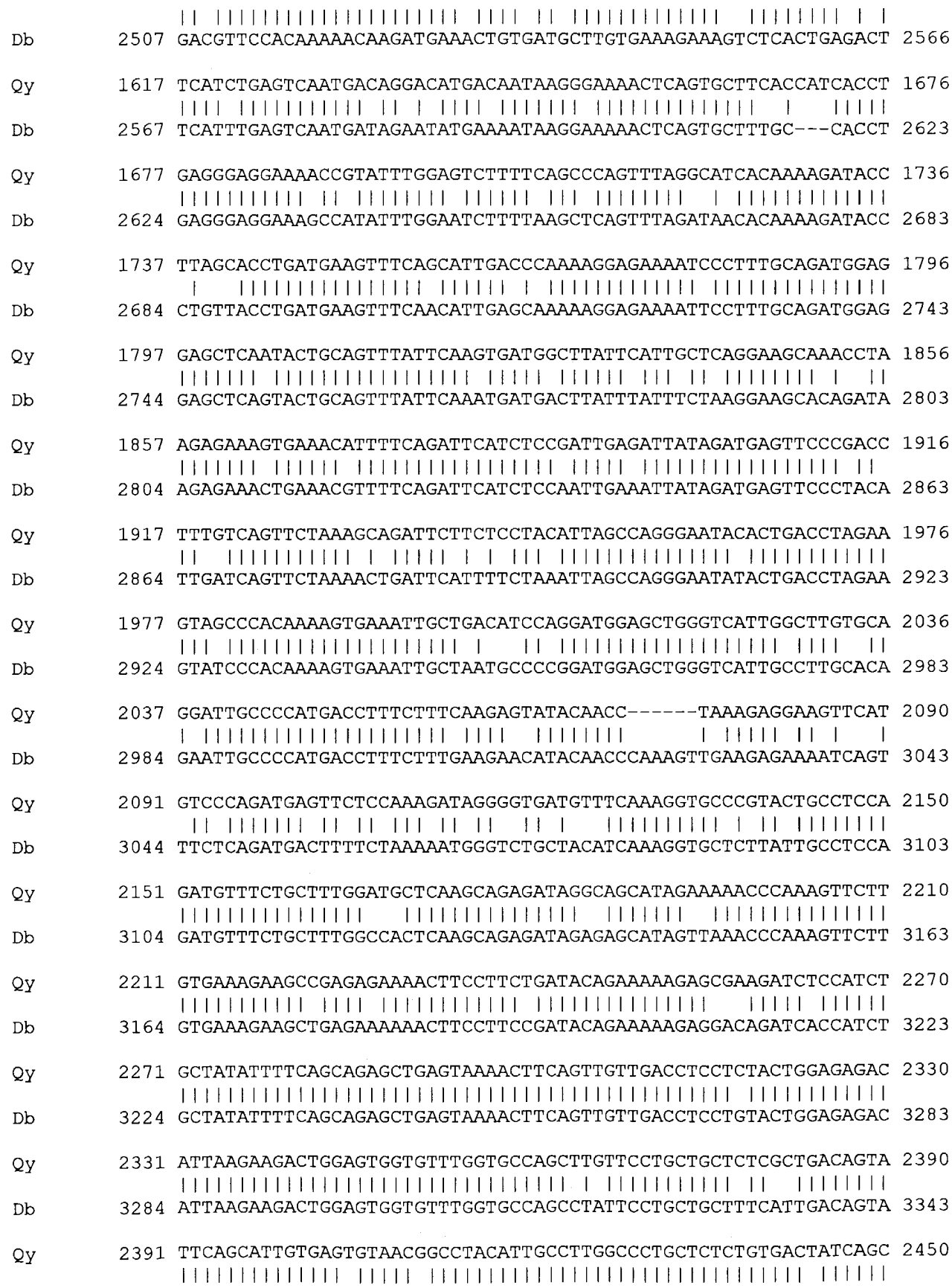

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              |||||||||||| |||||||||||||| |||||||||||||| |||||||||||||||||
Db       3404 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC 3463

Qy       2511 AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT 2570
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Db       3464 AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT 3523

Qy       2571 TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT 2630
              |||||||||||||||| |||||||| ||||| |||||||| ||||||||||||||||||
Db       3524 TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT 3583

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Db       3584 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 3643

Qy       2691 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT 2750
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Qy       2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
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Qy       3099 ATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATT 3158
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Db       4058 A--TCTTTTTCCTATCTGAGGCACTGGTGGA-----------ATAAAAAACCTGTATATT 4104

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Db       4165 AAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATG 4224
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Qy       3272 CAGATTTTCTGAAATGAAA----TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAA 3327
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Db       4225 CAGATTTTCTGAAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGAATGAC 4284

Qy       3328 AAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATTAATTG 3387
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Qy       3388 CCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTCACGAAGCTTAGCCC 3447
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Qy       3448 TTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT------TCTGTCATGGGTTTTATGT 3501
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RESULT 8
AR220865
LOCUS       AR220865                4822 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 106 from patent US 6426186.
ACCESSION   AR220865
VERSION     AR220865.1  GI:23327742
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4822)
  AUTHORS   Jones,K.A., Volkmuth,W. and Walker,M.G.
  TITLE     Bone remodeling genes
  JOURNAL   Patent: US 6426186-A 106 30-JUL-2002;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy        361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
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Qy        481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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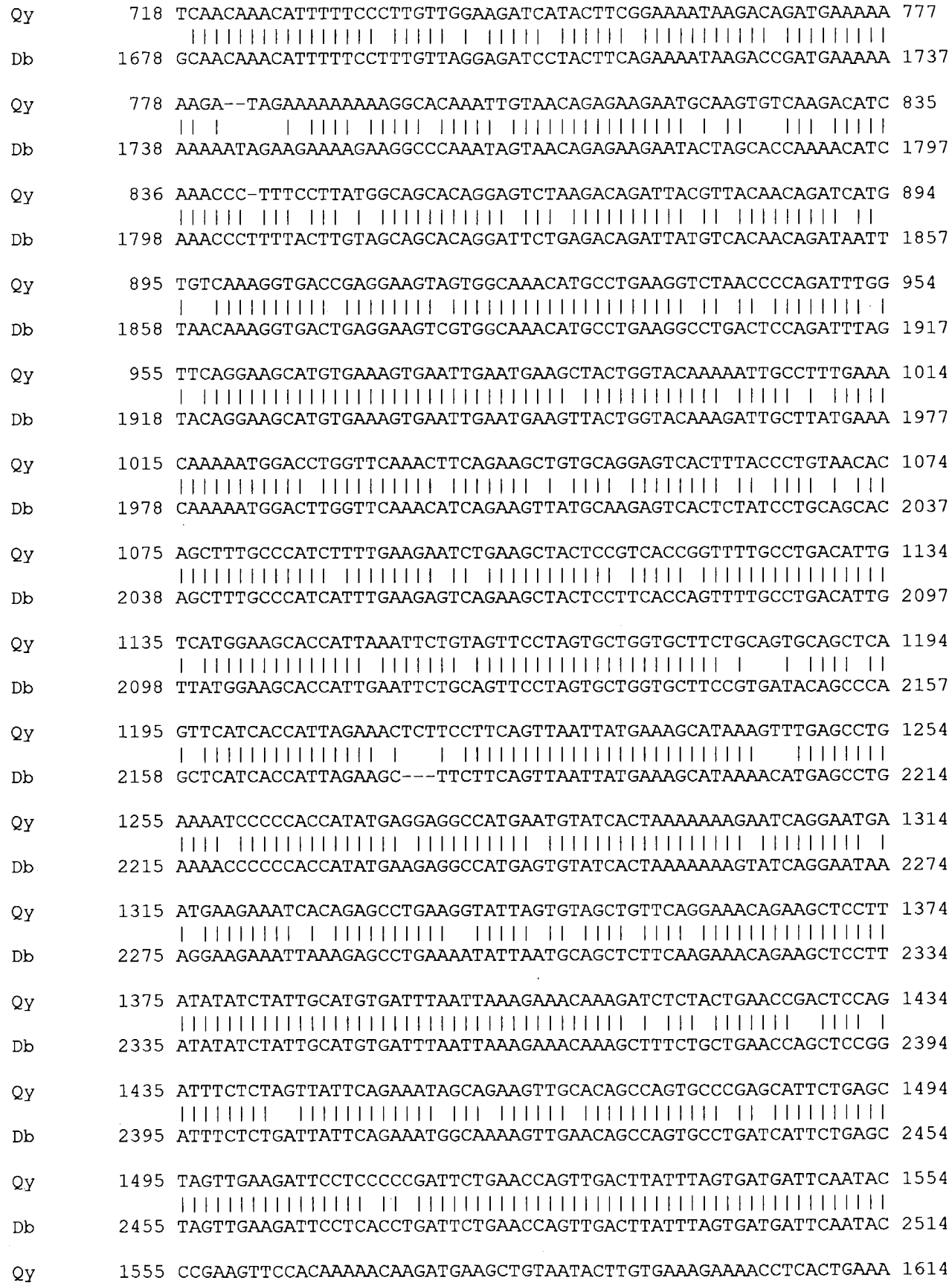

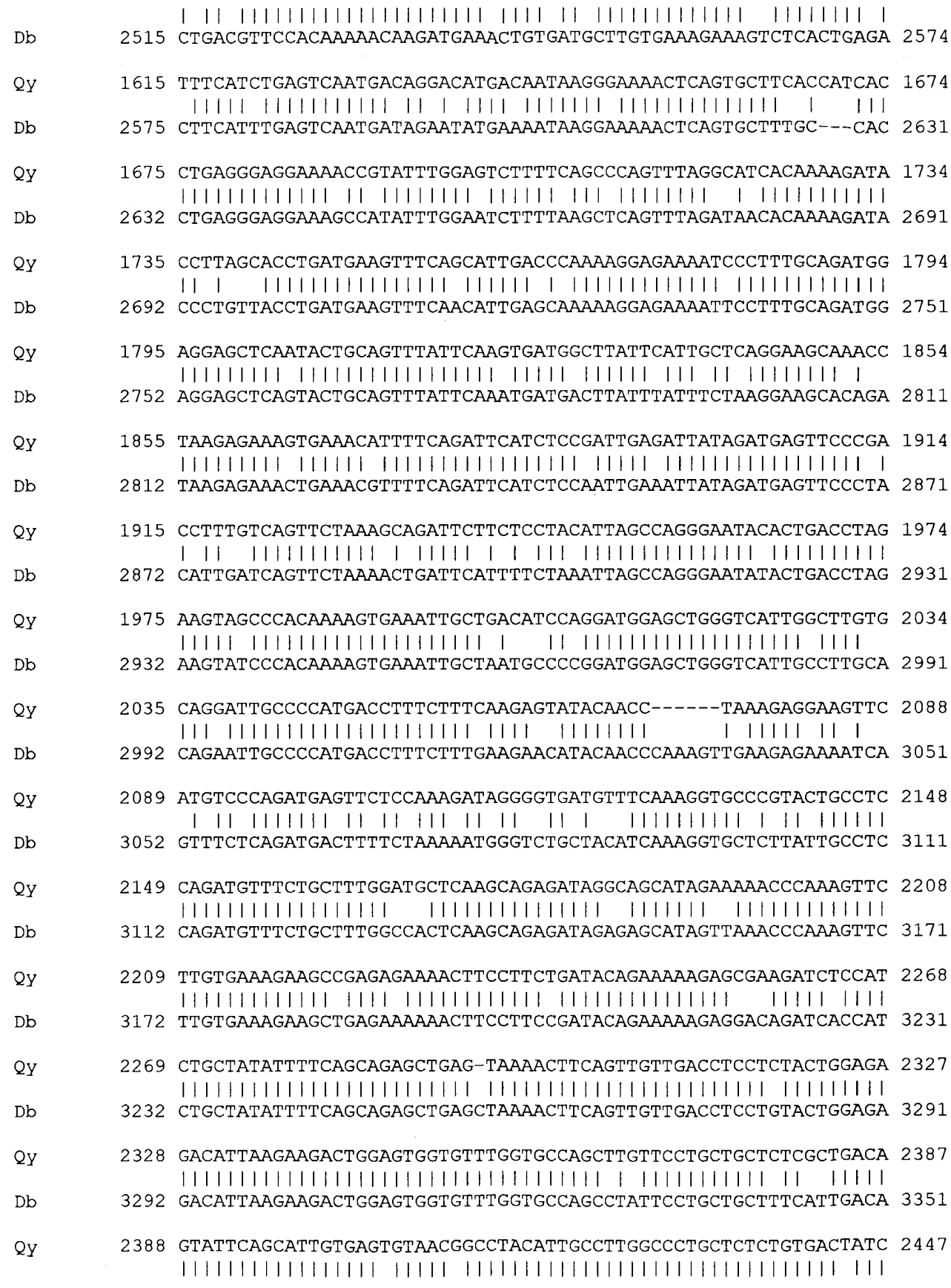

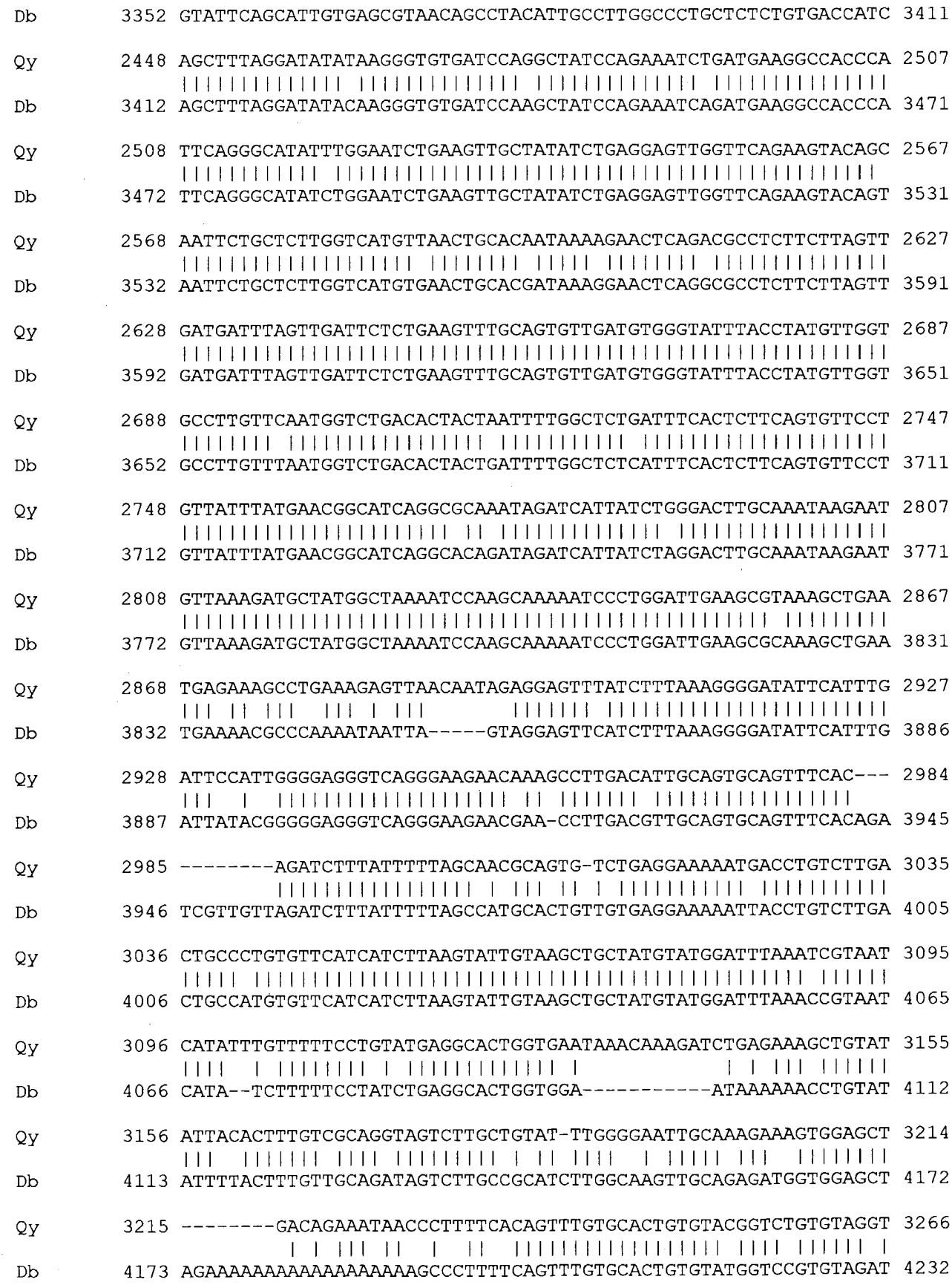

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Db       4233 TGATGCAGATTTTCTGAAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGA 4292

Qy       3323 GTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATT 3382
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Qy       3383 AATTGCCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTCACGAAGCTT 3442
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Db       4352 AATTGCCAATATAAGTAAATATAGATTATATATG------TATAGTGTTTCACAAAGCTT 4405

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Qy       3497 TATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCA 3556
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Db       4465 TACATGTGTAGTTCCAAAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCA 4524

Qy       3557 TCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTG 3615
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Qy       3616 CACAGACTTACTGTAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAA 3673
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Qy       3674 AAA-------TGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT--------AAAT 3718
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Db       4642 AAATGTTGTTTGTTTGCAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAAT 4701

Qy       3719 GACGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGA 3778
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Db       4702 GAAGATTTATACCATTGTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGA 4761

Qy       3779 ACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAAA 3833
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RESULT 9
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LOCUS       AF148537               4632 bp    mRNA    linear   PRI 09-SEP-2000
DEFINITION  Homo sapiens reticulon 4a mRNA, complete cds.
ACCESSION   AF148537
VERSION     AF148537.1  GI:10039550
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4632)
  AUTHORS   Yang,J., Yu,L., Bi,A.D. and Zhao,S.Y.
  TITLE     Assignment of the human reticulon 4 gene (RTN4) to chromosome
            2p14-->2p13 by radiation hybrid mapping
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  JOURNAL   Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
  MEDLINE   20237542
   PUBMED   10773680
REFERENCE   2  (bases 1 to 4632)
  AUTHORS   Zhou,Y., Yu,L. and Zhao,S.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of
            Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
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ORIGIN
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  Best Local Similarity   85.0%;  Pred. No. 0;
  Matches 3292;  Conservative    0;  Mismatches  442;  Indels  137;  Gaps   24;

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Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
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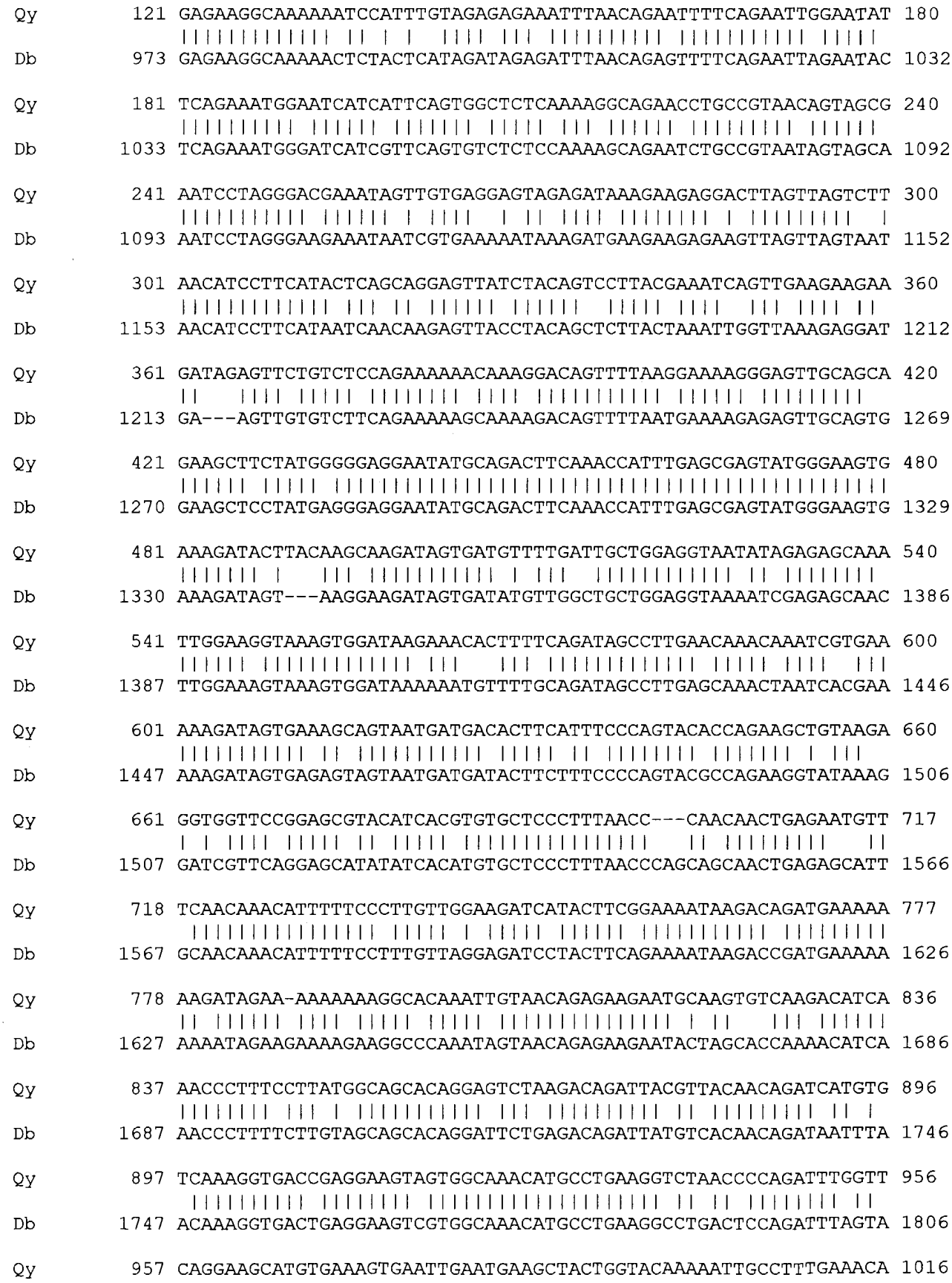

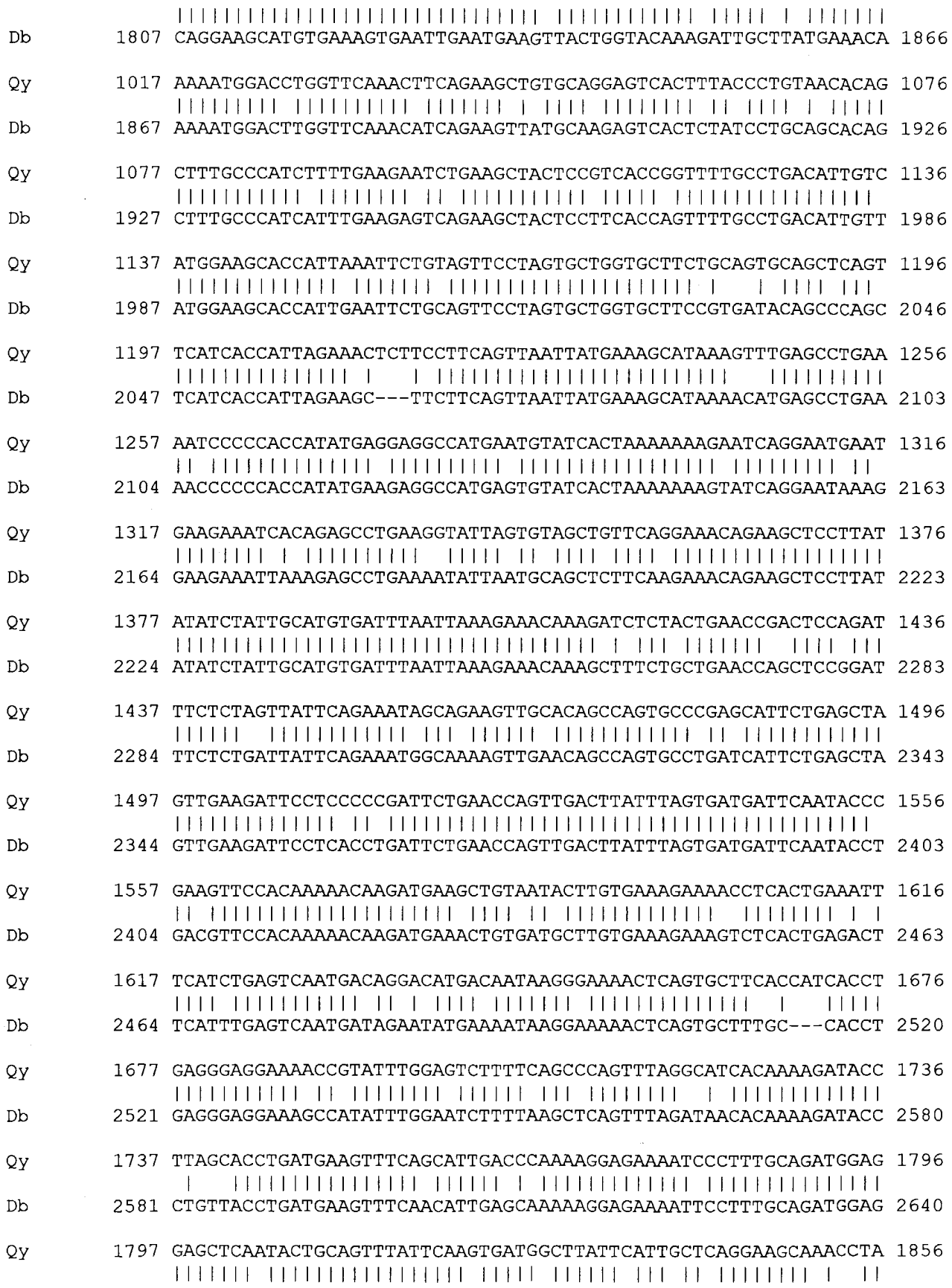

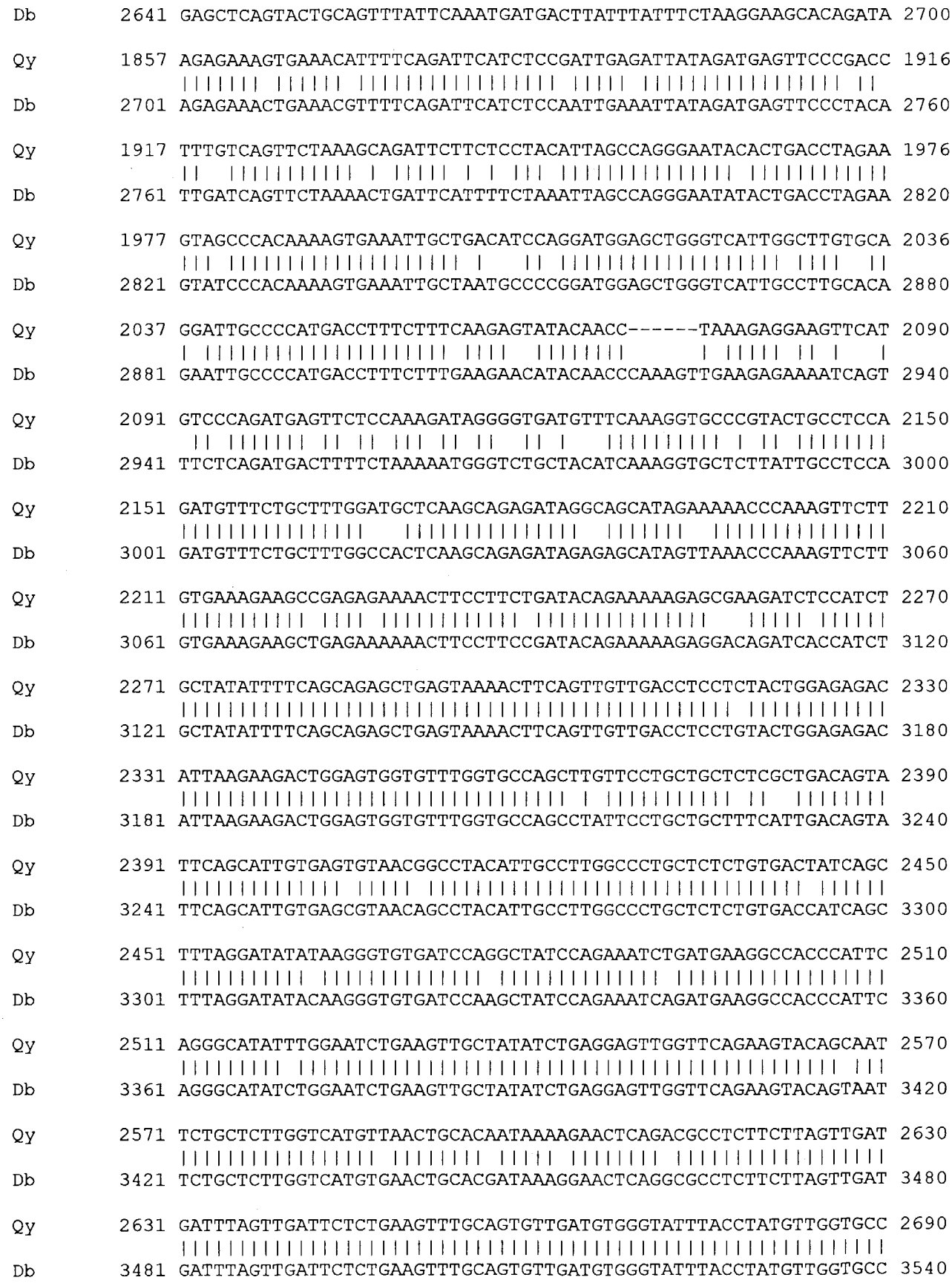

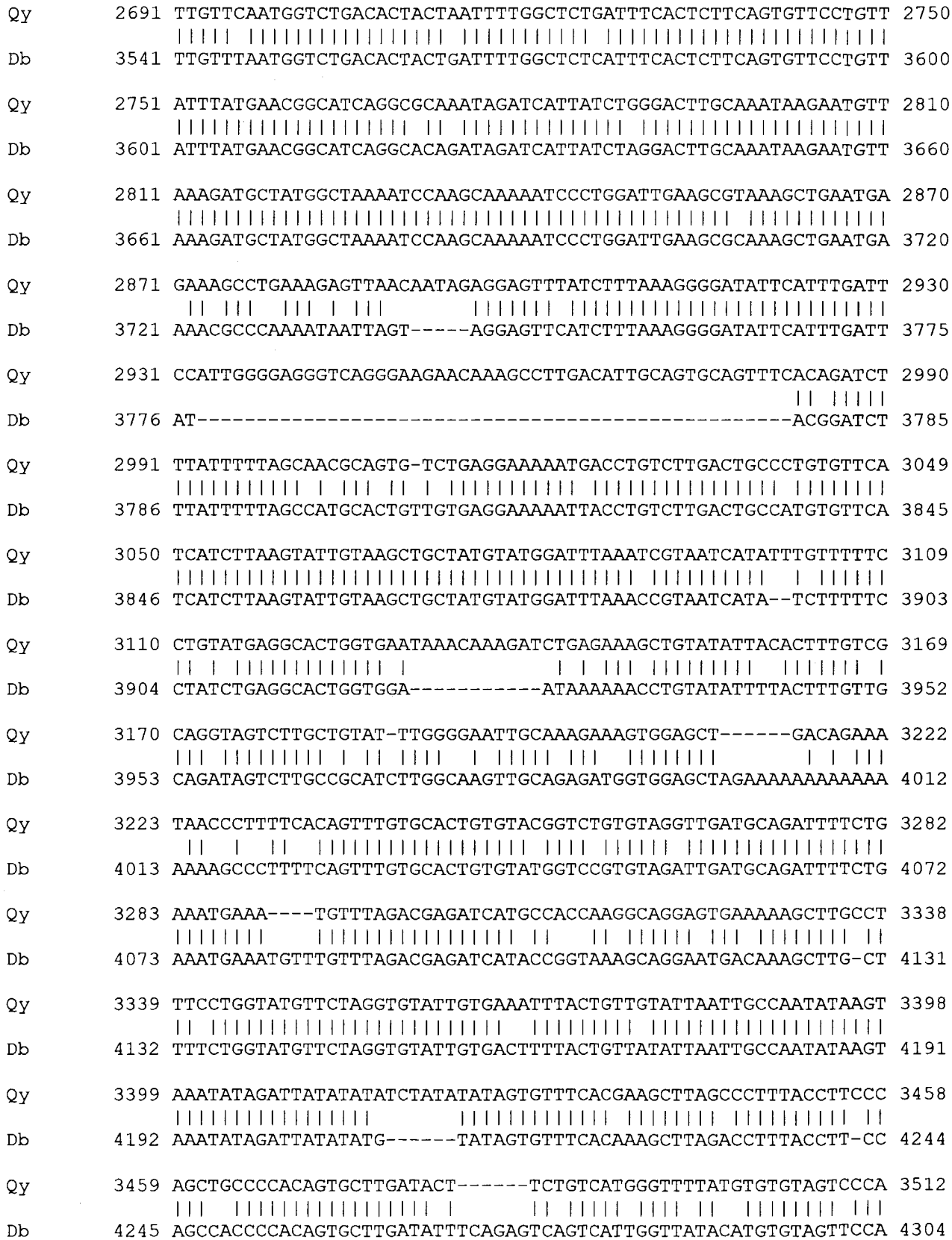

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Qy       3632 TTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA-------TGTTTG 3682
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Qy       3683 CAAATATCAAACATTGTTATGTAAGAAAATAT--------AAATGACGATTTATACAATT 3734
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Db       4482 CAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACCATT 4541

Qy       3735 GTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGT 3794
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RESULT 10
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LOCUS       AX195249                4053 bp    RNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 5 from Patent WO0151520.
ACCESSION   AX195249
VERSION     AX195249.1  GI:15385809
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Strittmatter,S.M.
  TITLE     Nogo receptor-mediated blockade of axonal growth
  JOURNAL   Patent: WO 0151520-A 5 19-JUL-2001;
            YALE UNIVERSITY (US)
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ORIGIN

Query Match 62.1%; Score 2379.4; DB 6; Length 4053;
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Qy        301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
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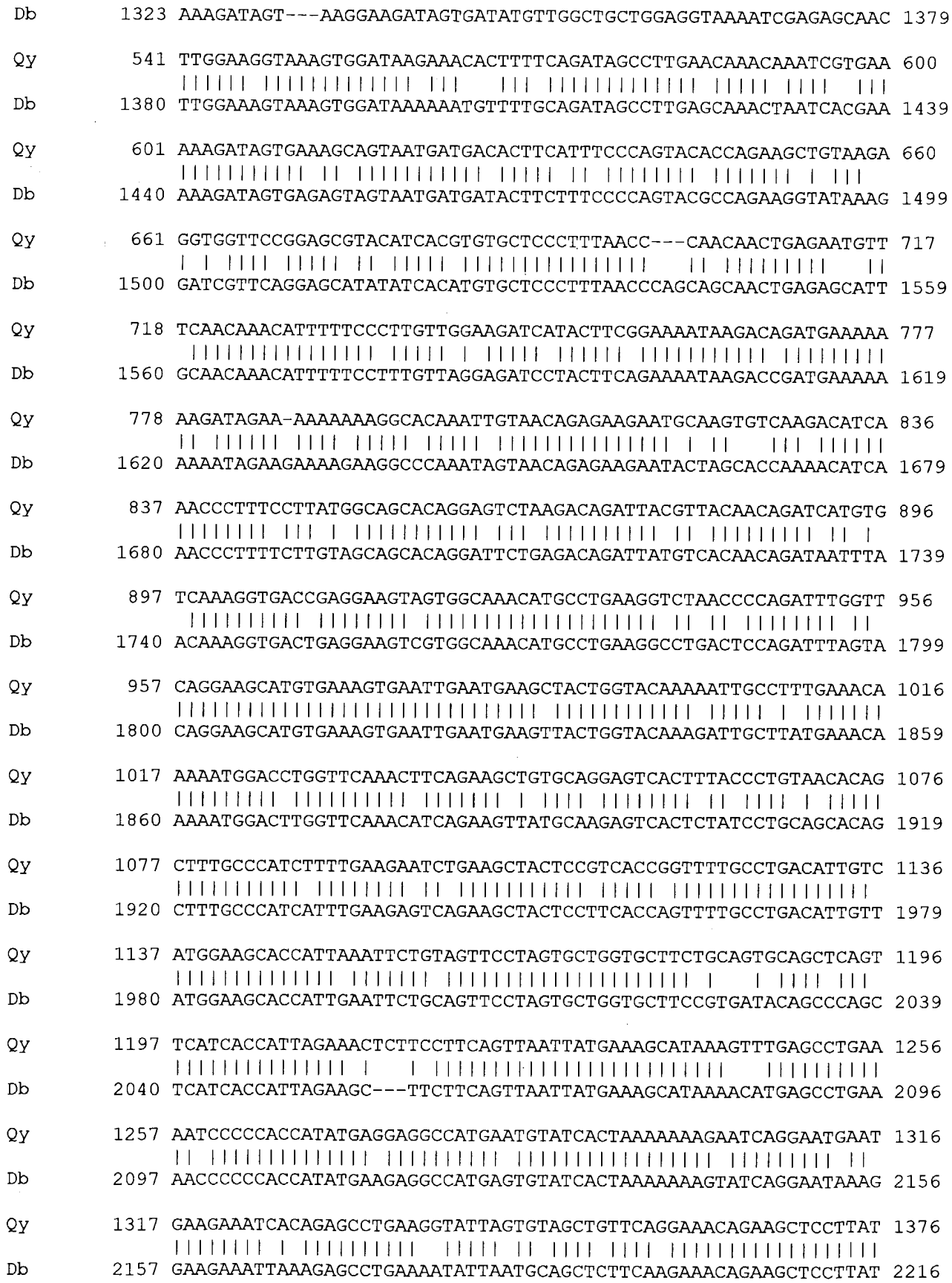

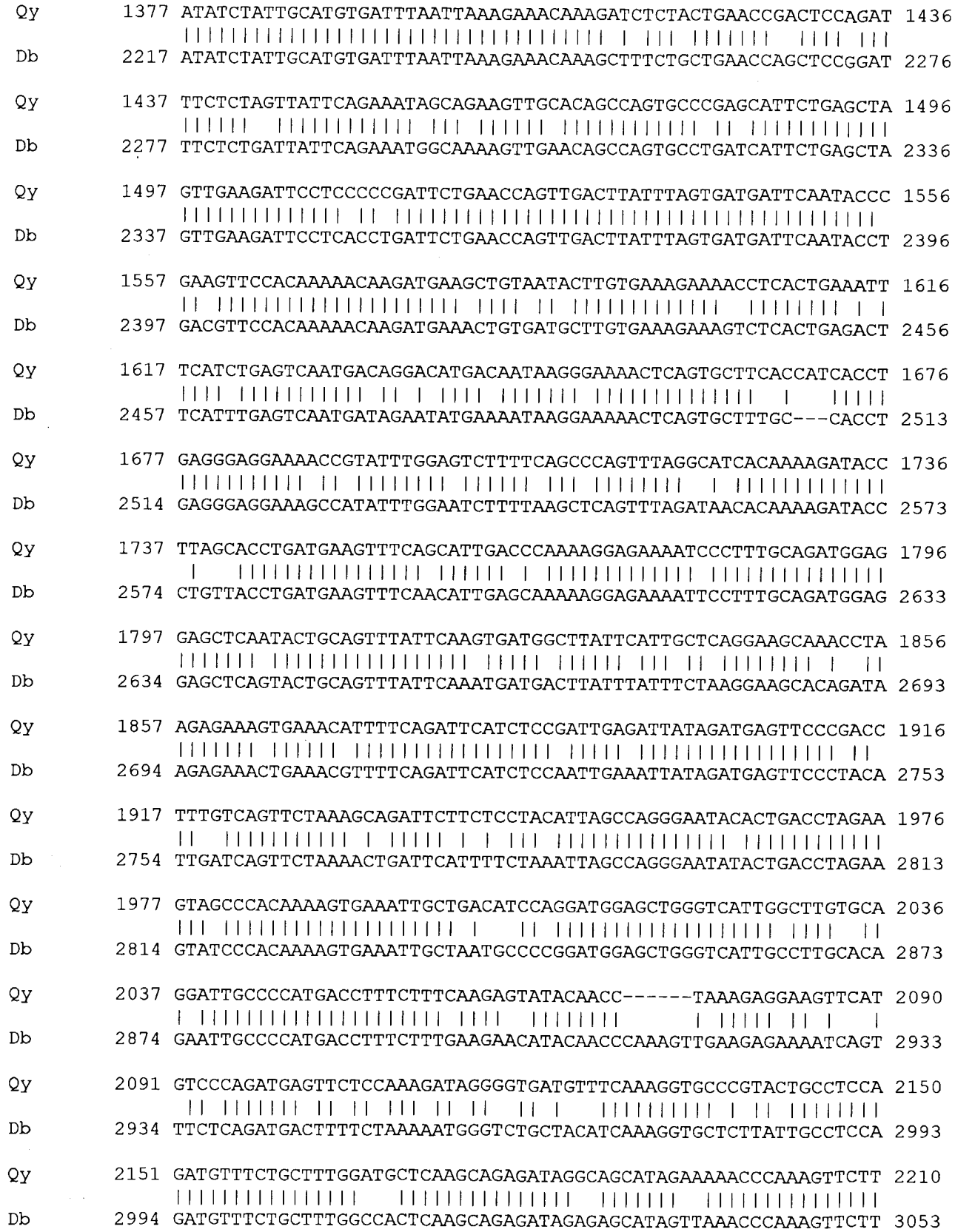

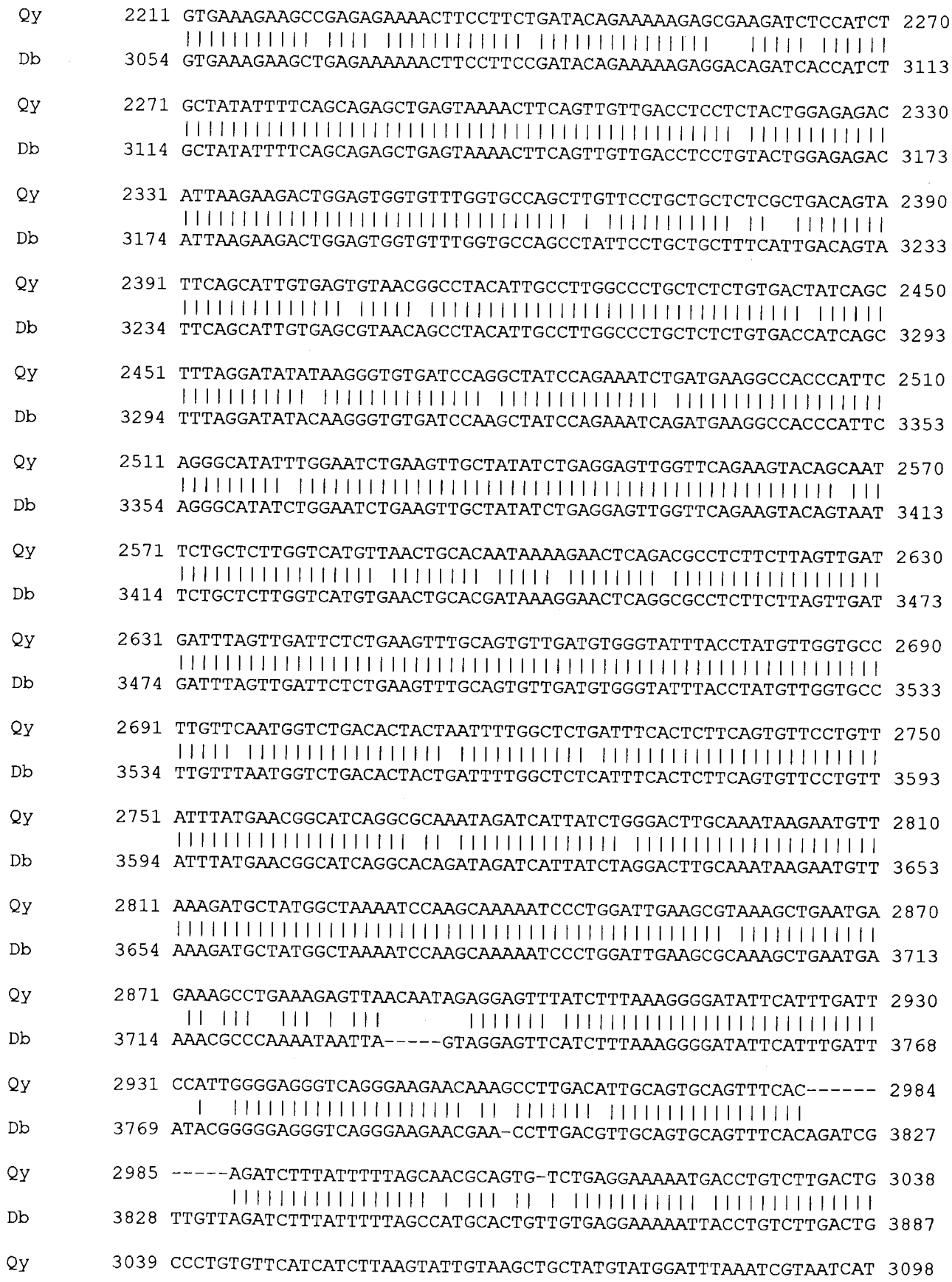

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RESULT 11
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LOCUS       AB020693               4053 bp    mRNA    linear   PRI 16-JUN-1999
DEFINITION  Homo sapiens mRNA for KIAA0886 protein, complete cds.
ACCESSION   AB020693
VERSION     AB020693.1  GI:4240260
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Hirosawa,M.,
            Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes.
            XII. The complete sequences of 100 new cDNA clones from brain which
            code for large proteins in vitro
  JOURNAL   DNA Res. 5 (6), 355-364 (1998)
  MEDLINE   99156230
   PUBMED   10048485
REFERENCE   2  (bases 1 to 4053)
  AUTHORS   Ohara,O., Suyama,M., Kikuno,R., Nagase,T. and Ishikawa,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-DEC-1998) Osamu Ohara, Kazusa DNA Research Institute,
            Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
            Fax:+81-438-52-3914)
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31 December 1998

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ORIGIN

Query Match 62.1%; Score 2379.4; DB 9; Length 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

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Db        846 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 905

Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
              ||| | |||||||||||||||||| || || |   | |||||||||||||   |||||
Db        906 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965

Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
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Db        966 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1025

Qy        181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
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Db       1026 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1085

Qy        241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
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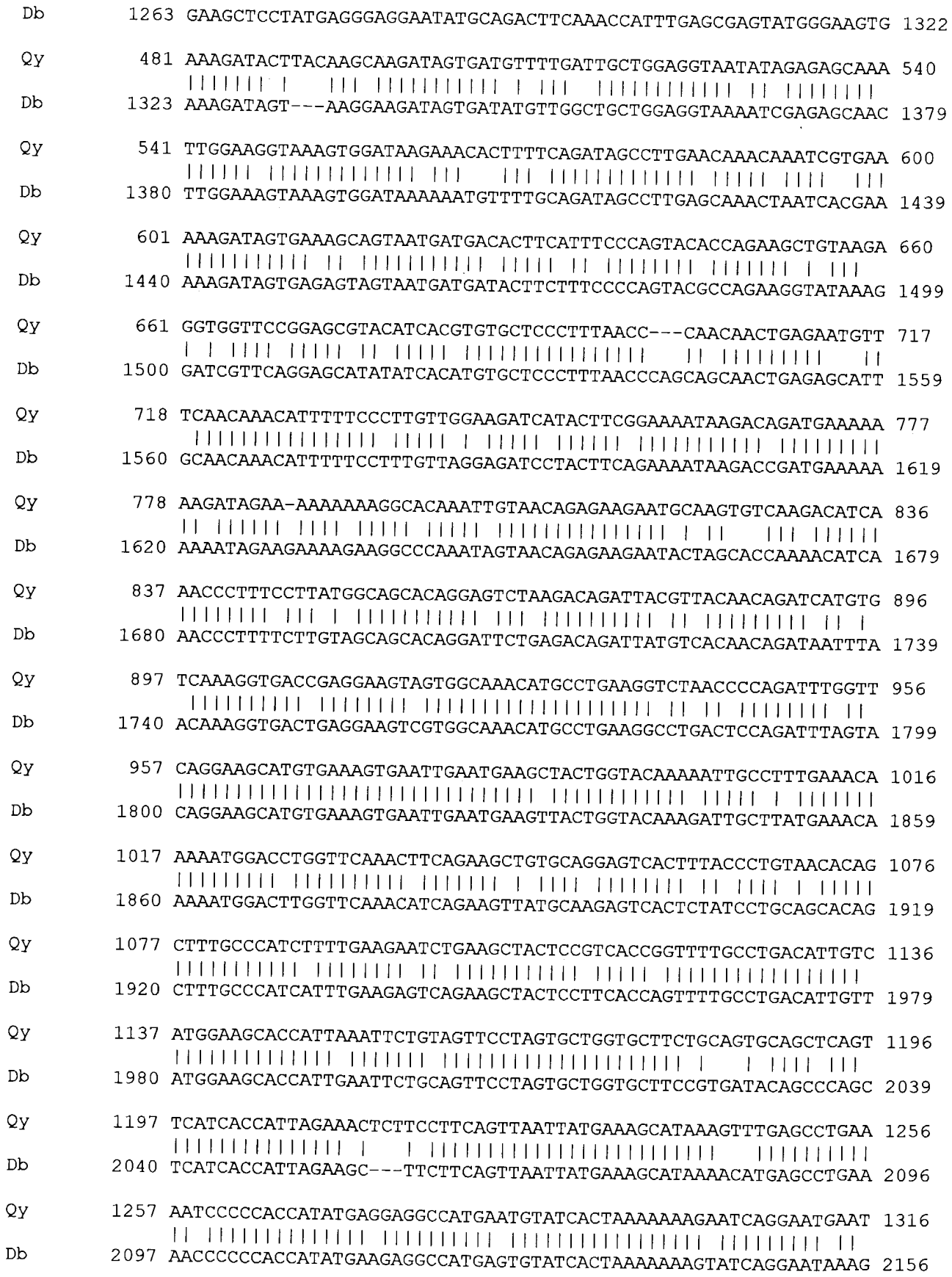

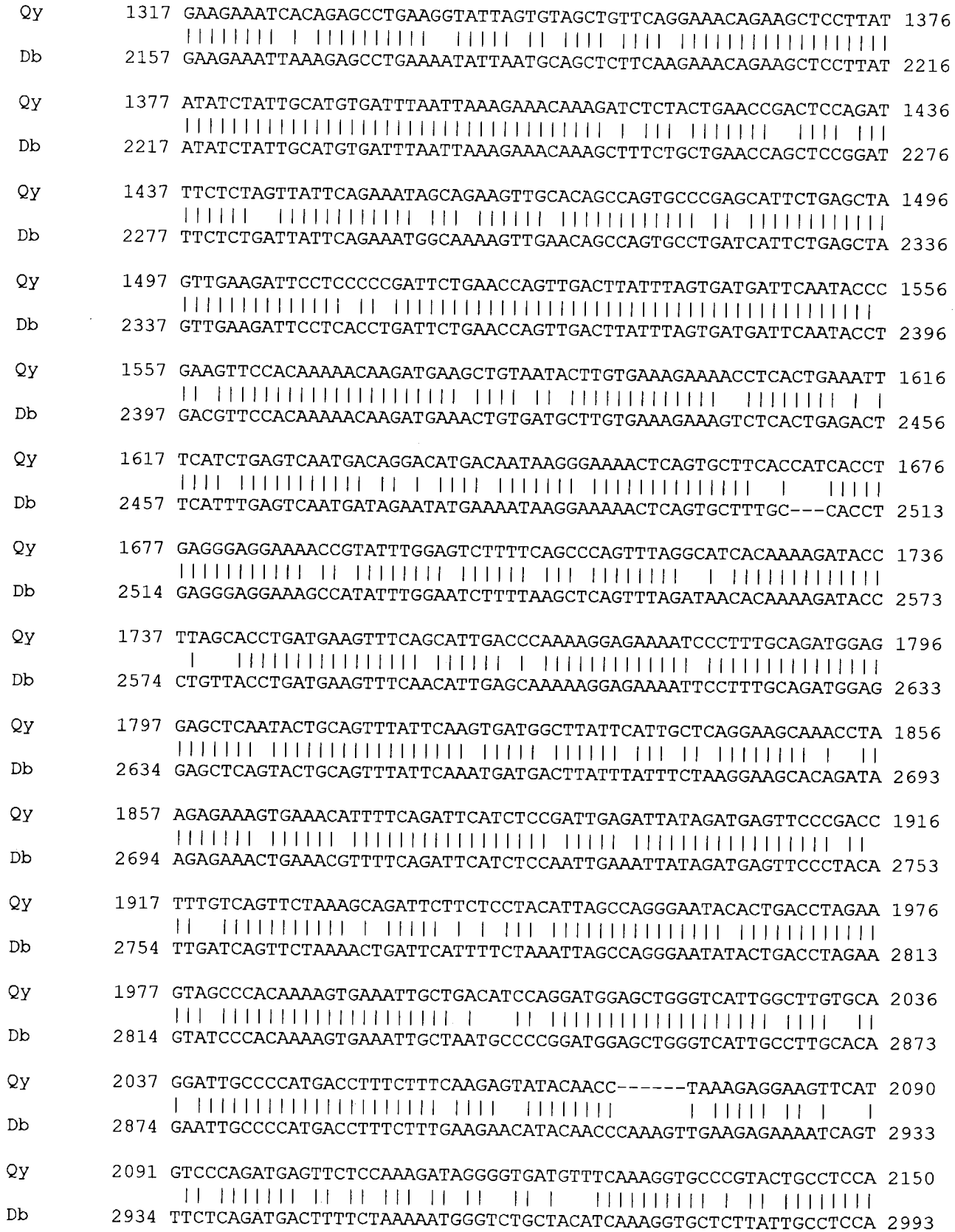

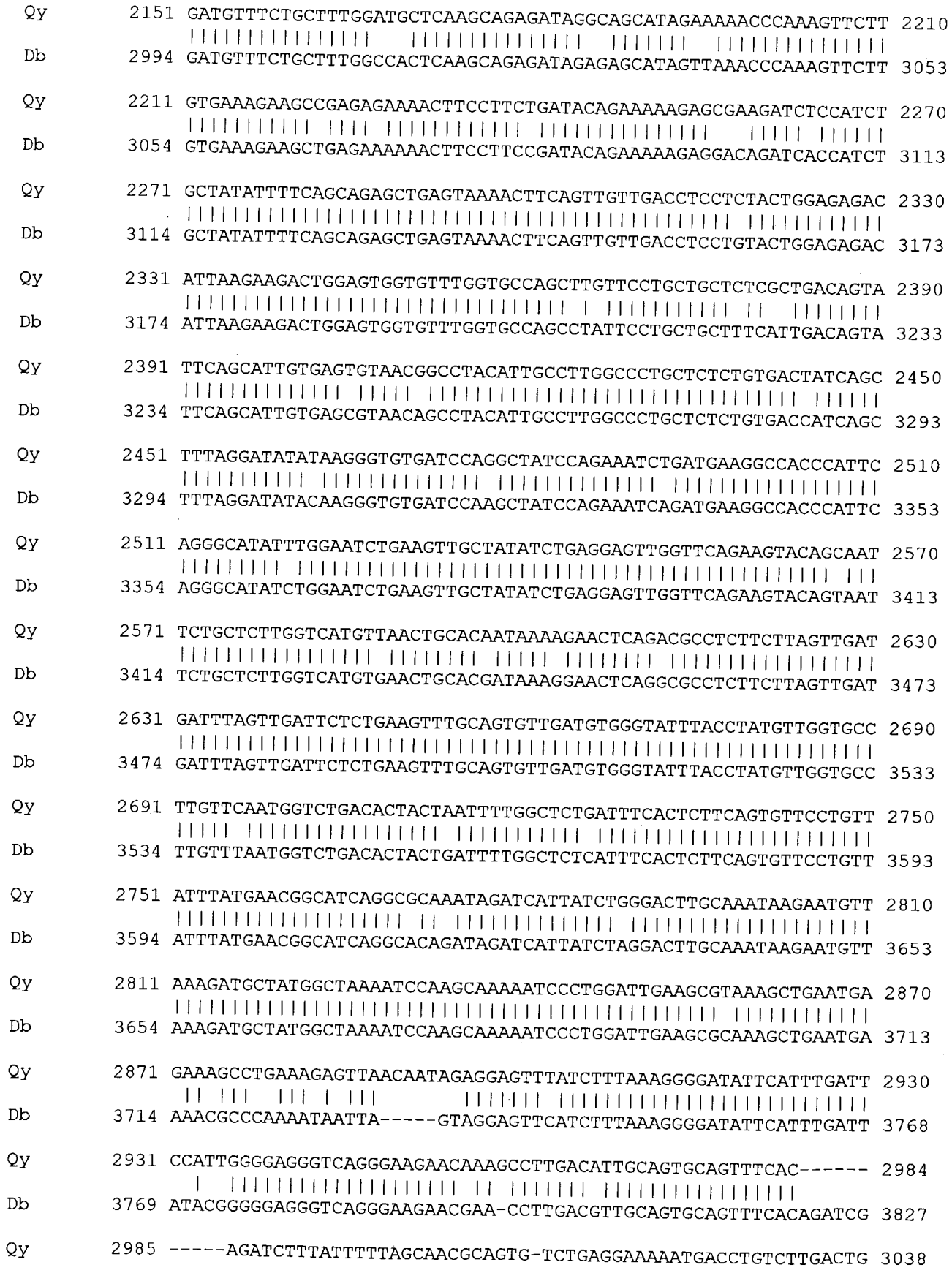

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Qy       3099 ATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATT 3158
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Qy       3159 ACACTTTGTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT 3214
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RESULT 12
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LOCUS AF333336 3491 bp mRNA linear PRI 27-MAY-2003
DEFINITION Homo sapiens testis specific reticulon 5 protein mRNA, complete cds.
ACCESSION AF333336
VERSION AF333336.1 GI:13377627
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3491)
AUTHORS Zhou,Z.M., Sha,J.H., Li,J.M., Lin,M., Zhu,H., Zhou,Y.D., Wang,L.R., Zhu,H., Wang,Y.Q. and Zhou,K.Y.
TITLE Expression of a novel reticulon-like gene in human testis
JOURNAL Reproduction 123 (2), 227-234 (2002)
MEDLINE 21857060
PUBMED 11866689
REFERENCE 2 (bases 1 to 3491)
AUTHORS Sha,J.H., Zhou,Z.M. and Li,J.M.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-2001) Key Lab of Reproductive Medicine, Nanjing Medical University, Han Zhong Road 140, Nanjing, Jiangsu 210029, China
FEATURES Location/Qualifiers
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polyA_signal 3402. .3407

ORIGIN

Query Match 62.1%; Score 2379.2; DB 9; Length 3491;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 2806; Conservative 0; Mismatches 388; Indels 54; Gaps 14;

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Qy        241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
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Qy        421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
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Qy        481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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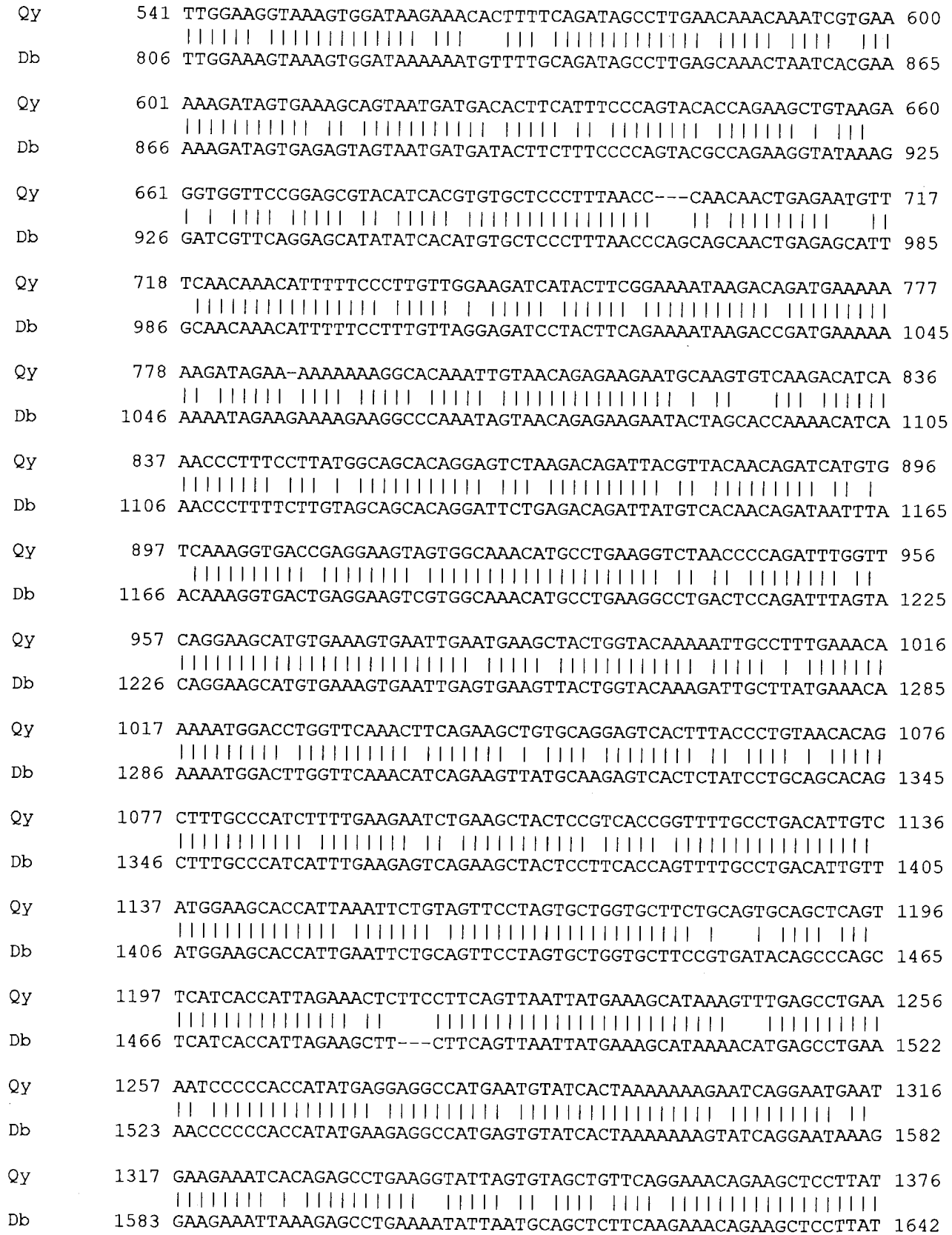

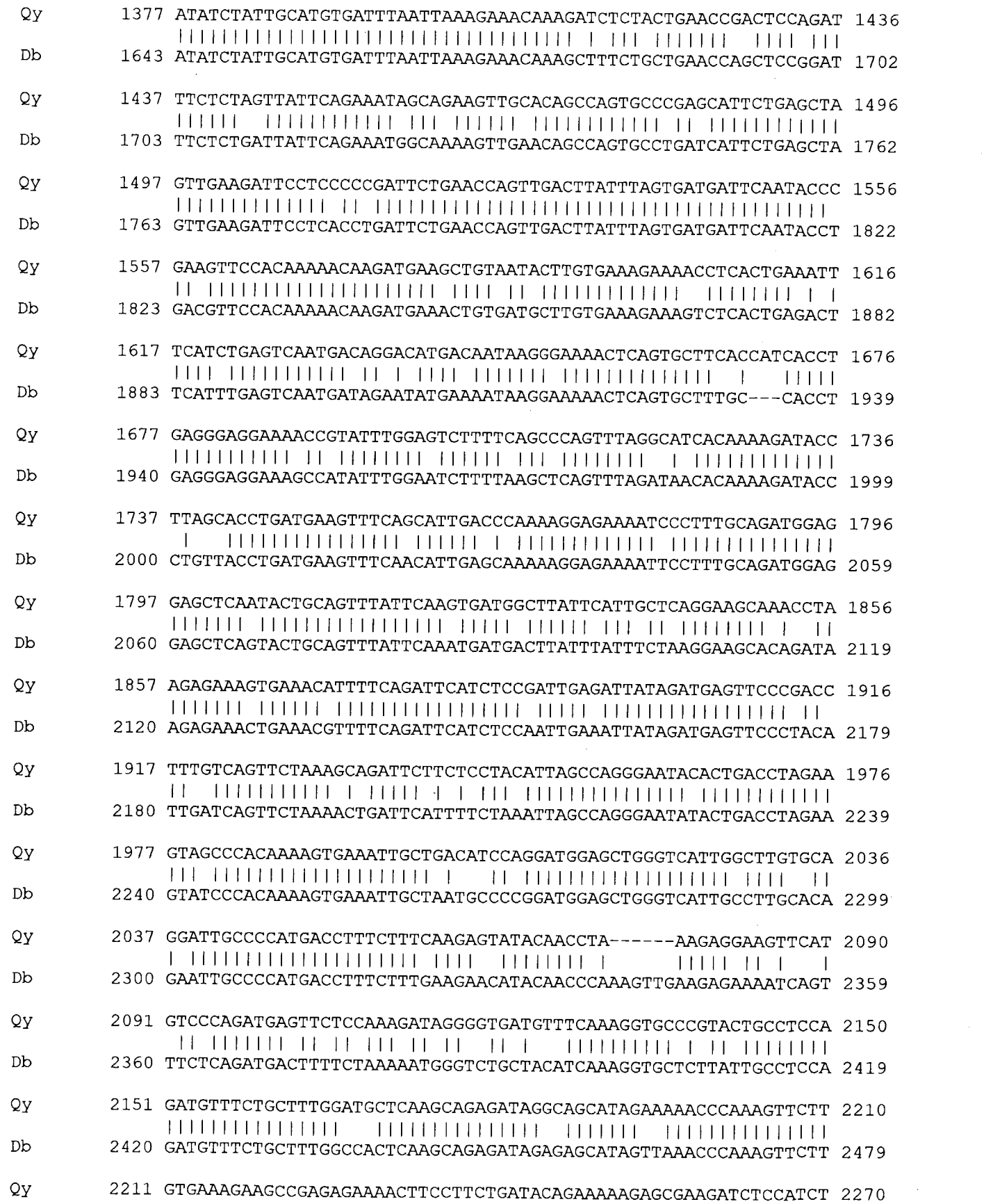

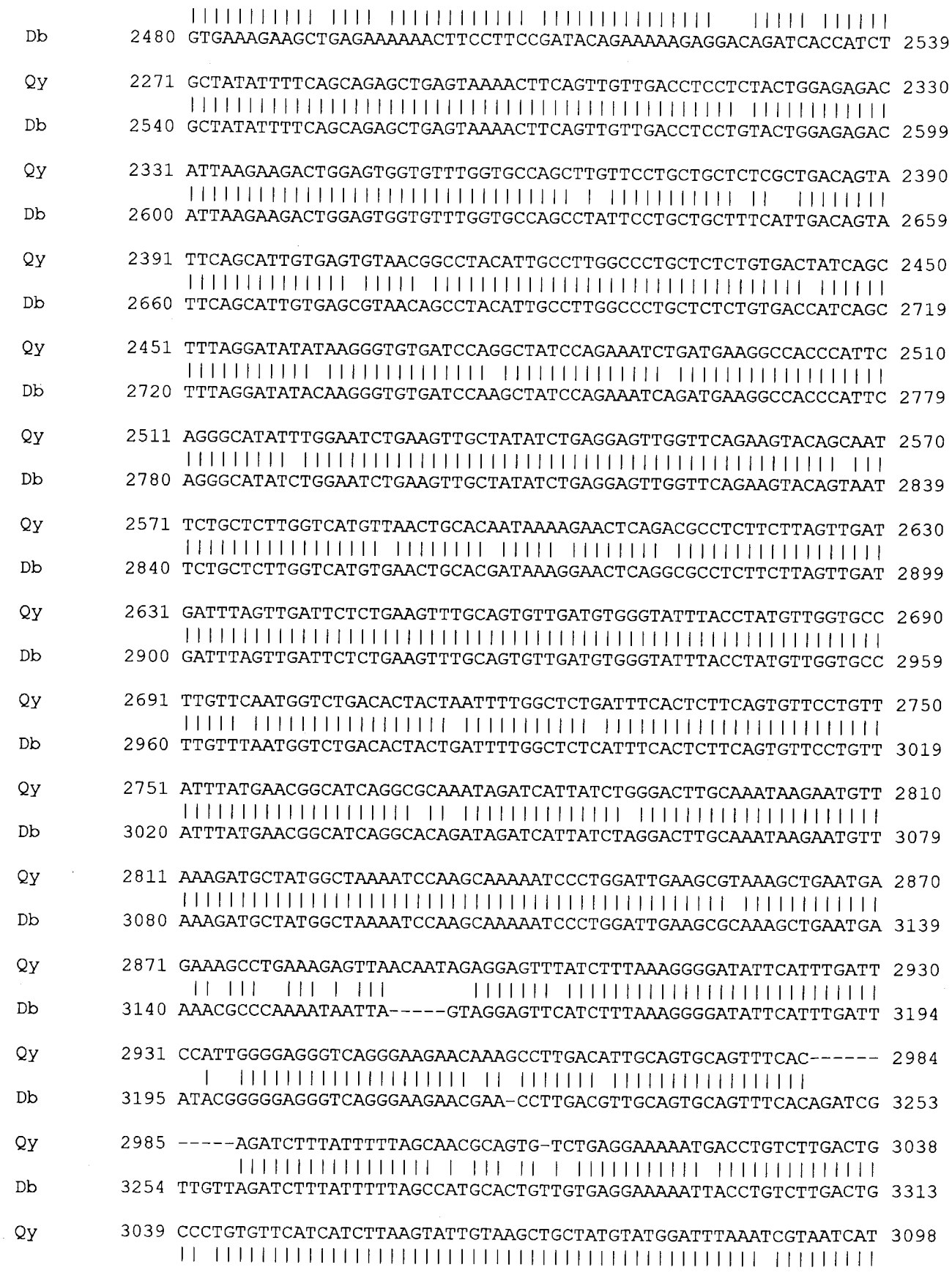

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Db       3421 TTACTTTGTTGCAGATAGTCTTGCCGCATCTGGGCAAGTTGCAAAAATGGTGGAGTTAAA 3480

Qy       3218 AGAAATAA 3225
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Db       3481 AAAAAAAA 3488
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LOCUS       AB040462                4166 bp    mRNA    linear   PRI 10-OCT-2001
DEFINITION  Homo sapiens mRNA for RTN-xL, complete cds.
ACCESSION   AB040462
VERSION     AB040462.1  GI:11610574
KEYWORDS    reticulon.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tagami,S., Eguchi,Y., Kinoshita,M., Takeda,M. and Tsujimoto,Y.
  TITLE     A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
            endoplasmic reticulum and reduces their anti-apoptotic activity
  JOURNAL   Oncogene 19 (50), 5736-5746 (2000)
  MEDLINE   21010696
   PUBMED   11126360
REFERENCE   2  (bases 1 to 4166)
  AUTHORS   Eguchi,Y., Tagami,S. and Tsujimoto,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate
            School of Medicine, Biomedical Research Center, Department of
            Medical Genetics; Yamadaoka 2-2, Suita, Osaka 567-0871, Japan
            (E-mail:eguchi@gene.med.osaka-u.ac.jp, Tel:+81-6-6879-3363,
            Fax:+81-6-6879-3369)
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ORIGIN

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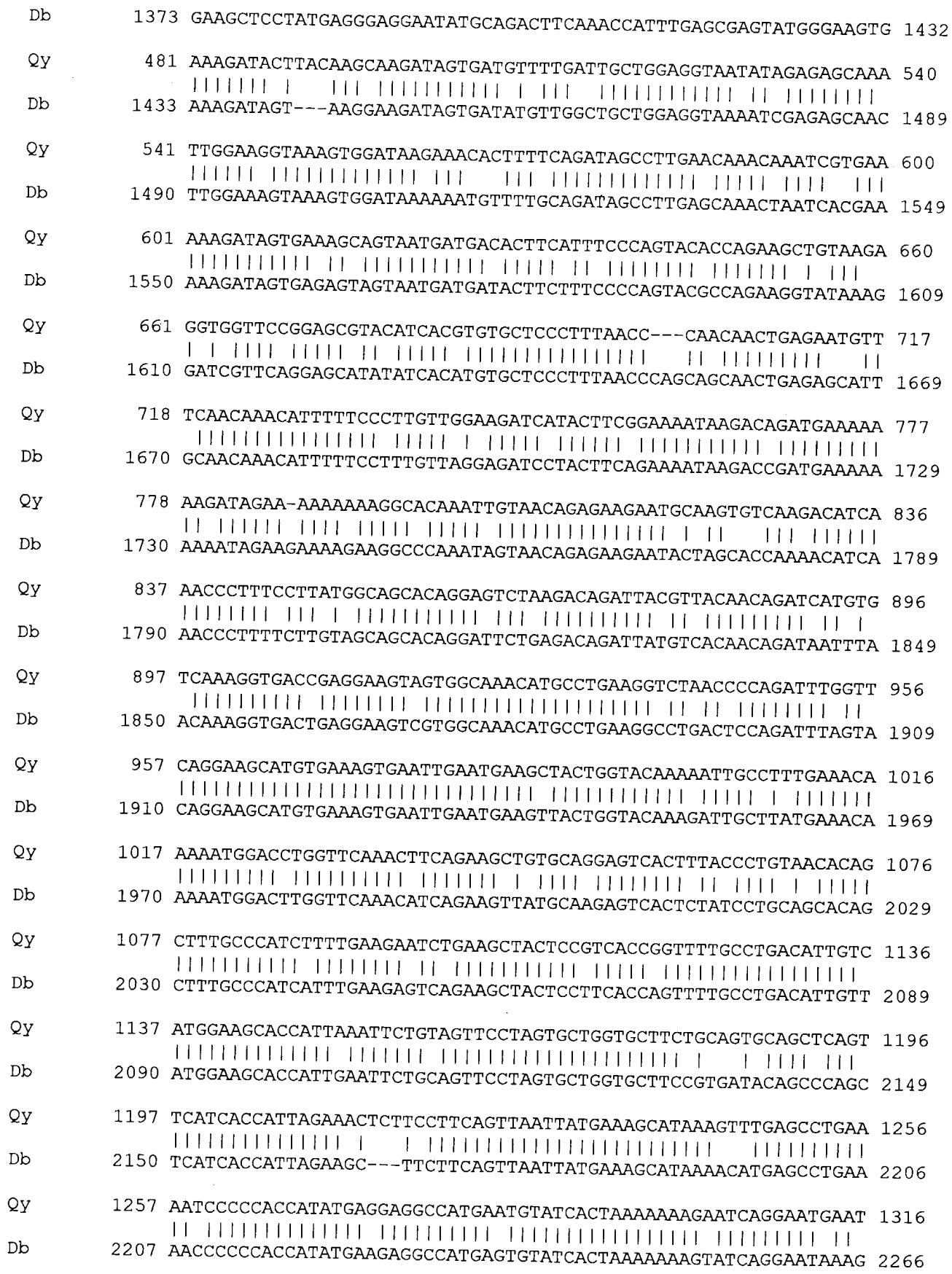

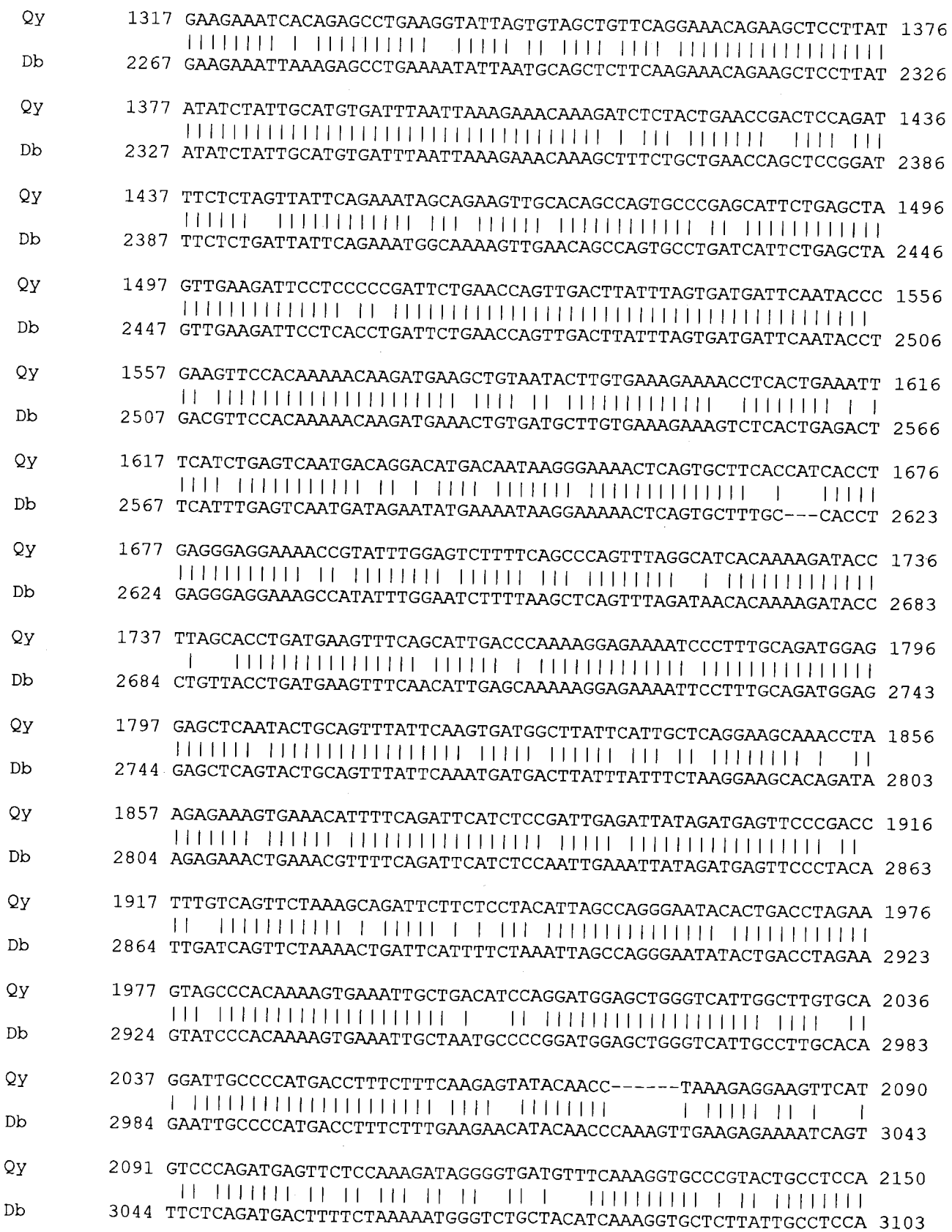

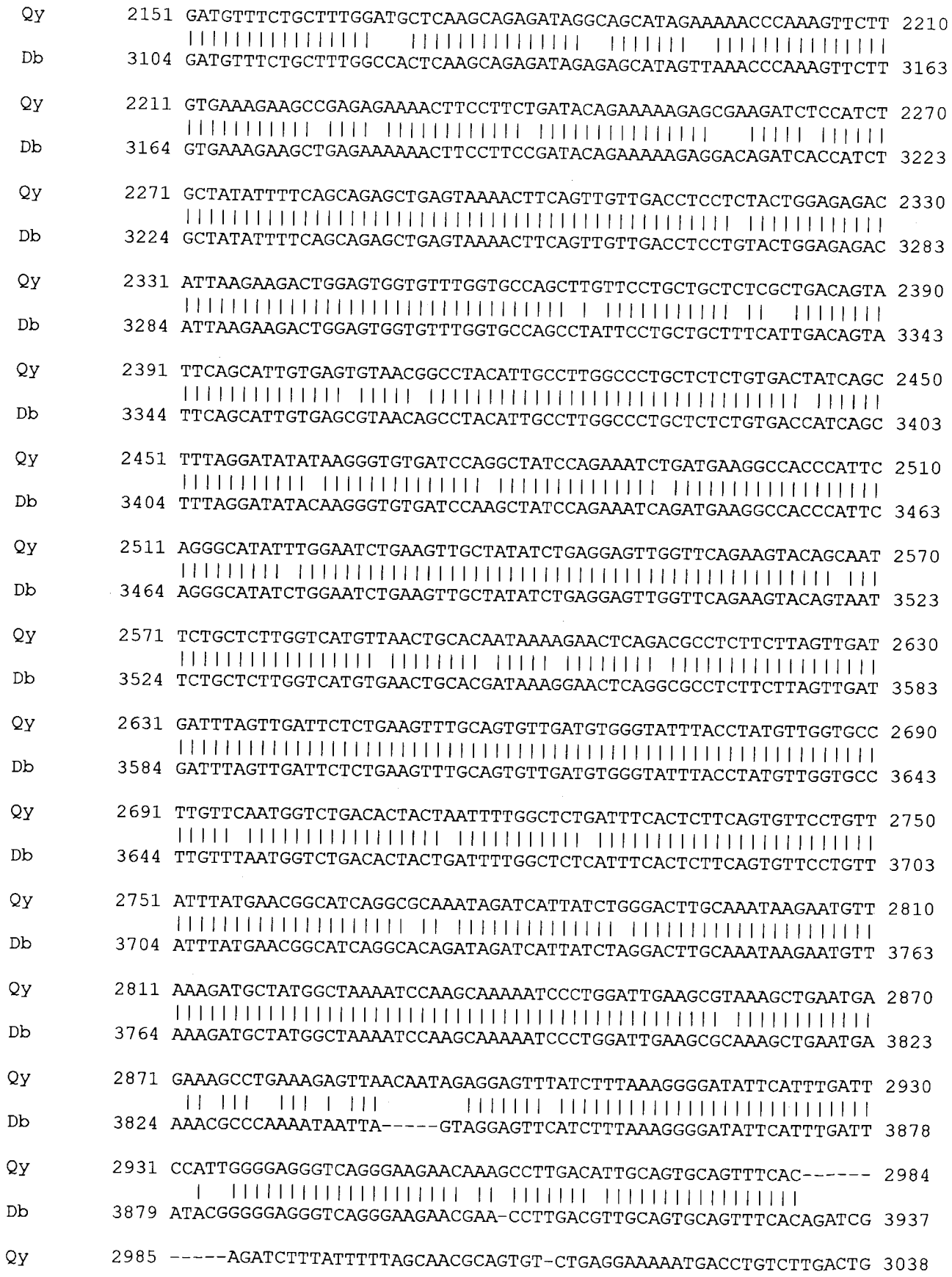
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RESULT 14
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LOCUS       BD270070                4093 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Secreted proteins and polynucleotides encoding them.
ACCESSION   BD270070
VERSION     BD270070.1  GI:33079838
KEYWORDS    JP 2002537757-A/32.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4093)
  AUTHORS   Valenzuela,D., Yuan,O., Hoffman,H., Hall,J. and Rapiejko,P.
  TITLE     Secreted proteins and polynucleotides encoding them
  JOURNAL   Patent: JP 2002537757-A 32 12-NOV-2002;
            ALPHAGENE INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002537757-A/32
            PD   12-NOV-2002
            PF   24-AUG-1999 JP 2000566287
            PR   24-AUG-1998 US    60/097638,24-AUG-1998 US    60/097659 PR
            09-SEP-1998 US    60/099618,28-SEP-1998 US    60/102092 PR
            25-NOV-1998 US    60/109978,23-DEC-1998 US    60/113645 PR
            23-DEC-1998 US    60/113646,23-AUG-1999 US    09/379246 PI   DARIO
            VALENZUELA,OLIVE YUAN,HEIDI HOFFMAN,JEFF HALL,PETER  PI   RAPIEJKO
            PC   C12N15/09,A61K38/00,A61K48/00,A61P3/10,A61P11/06,A61P21/00, PC
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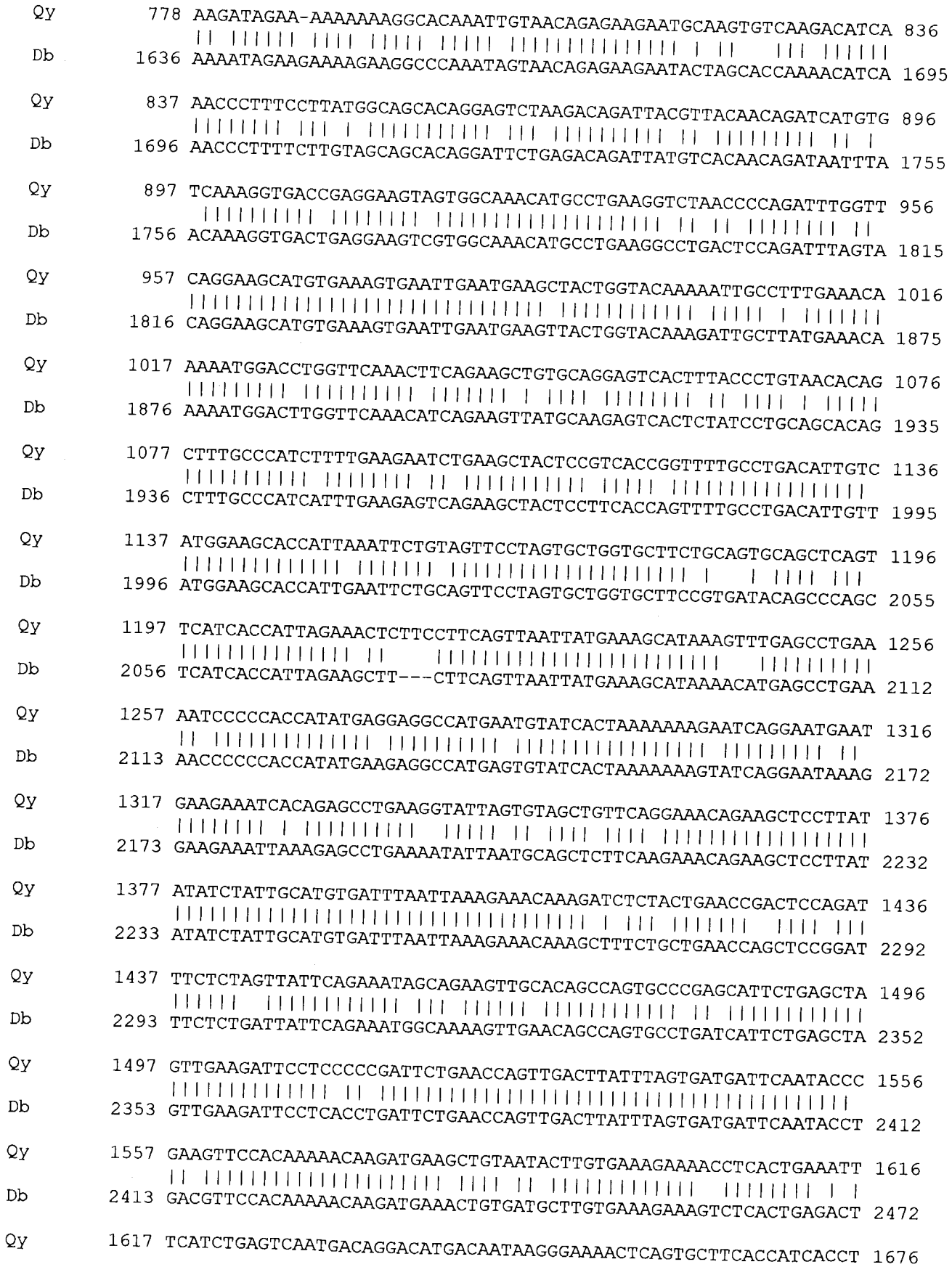

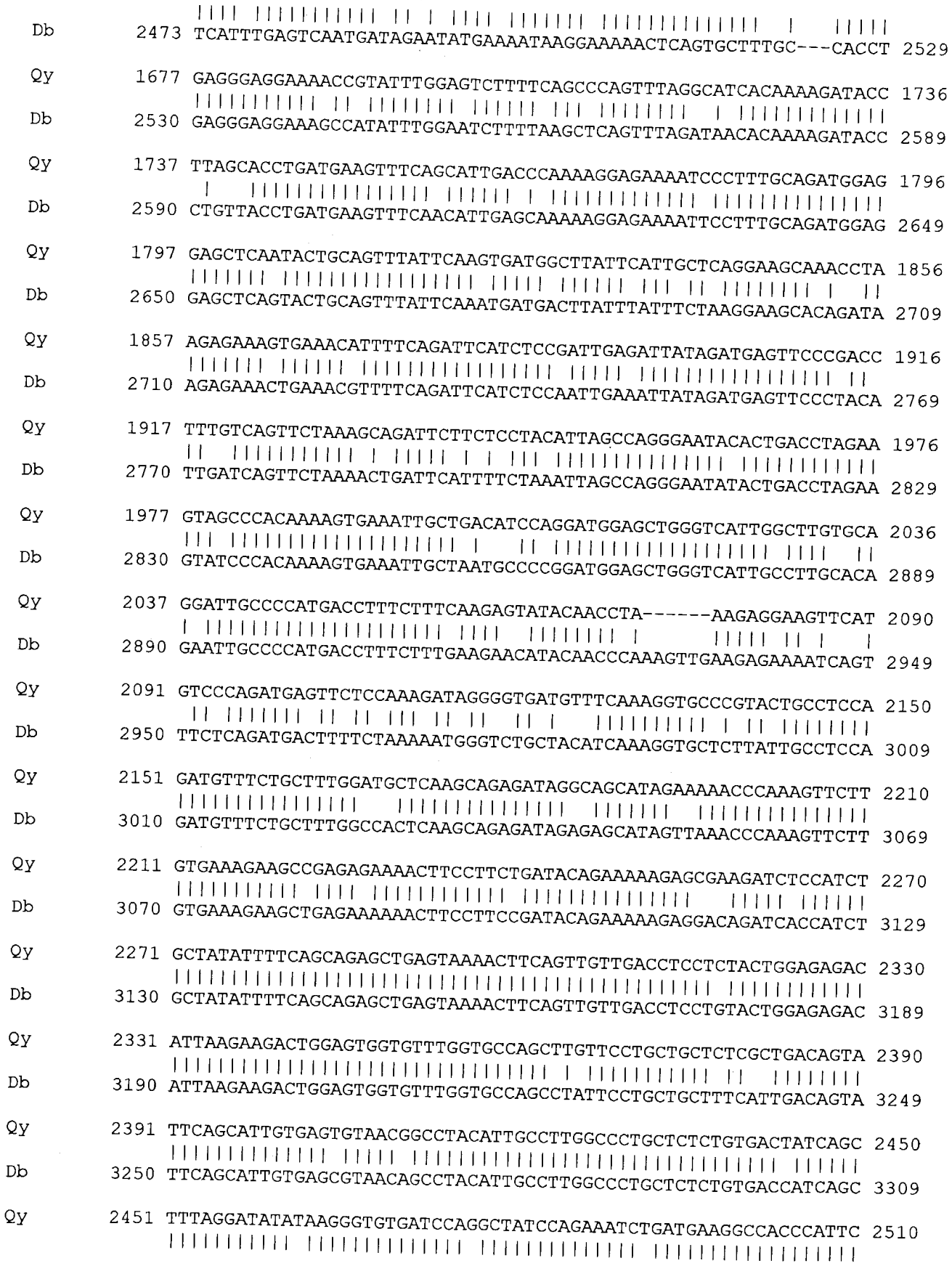

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RESULT 15
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DEFINITION  Protein similar to neuroendrocrine-specific protein, and encoding
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ACCESSION   BD249446
VERSION     BD249446.1  GI:33059216
KEYWORDS    JP 2002522016-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3579)
  AUTHORS   Michalovich,D. and Prinjha,R.K.
  TITLE     Protein similar to neuroendrocrine-specific protein, and encoding
  JOURNAL   Patent: JP 2002522016-A 1 23-JUL-2002;
            SMITHKLINE BEECHAM PLC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002522016-A/1
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            DAVID MICHALOVICH,RABINDER KUMAR PRINJHA
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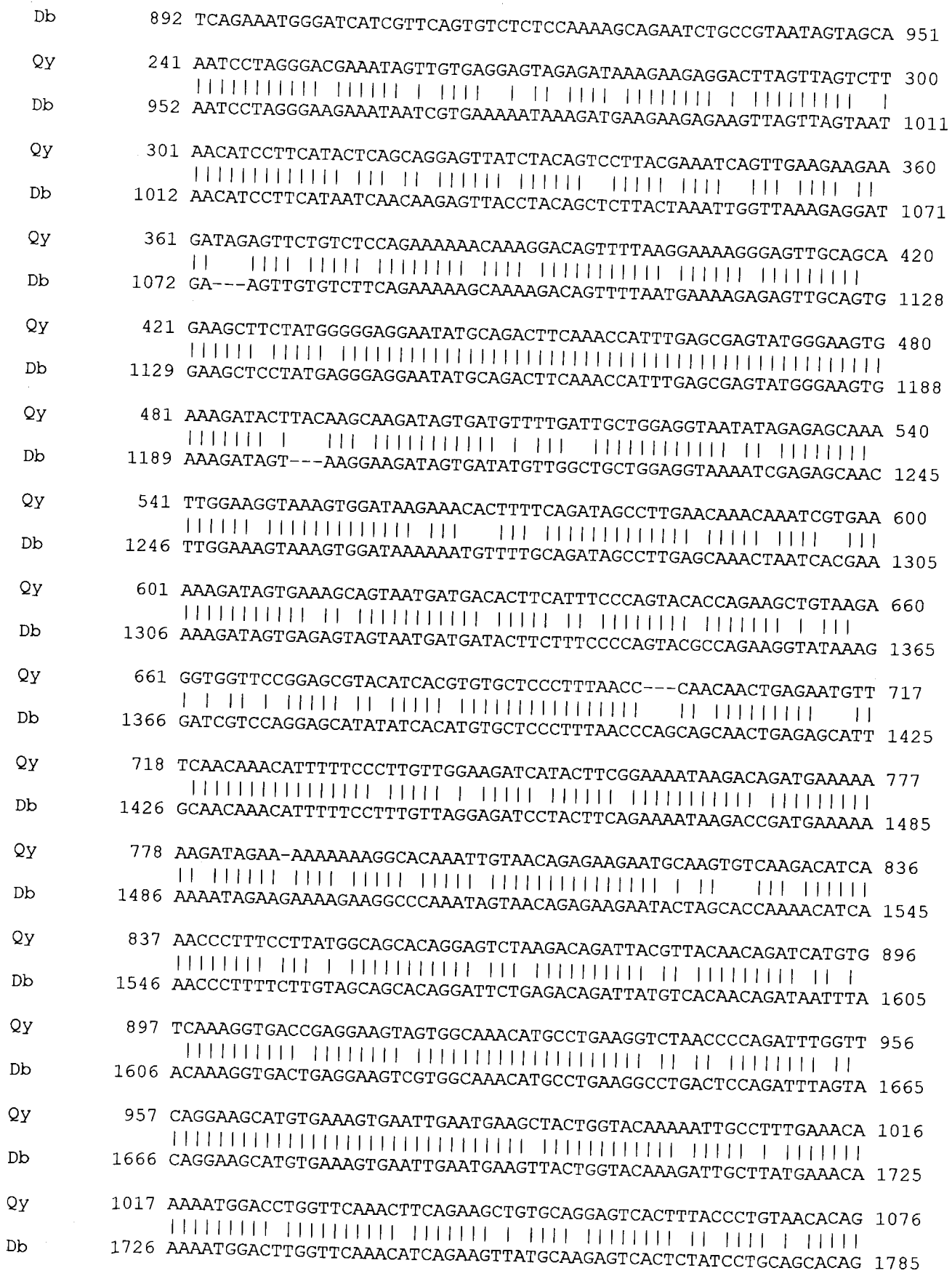

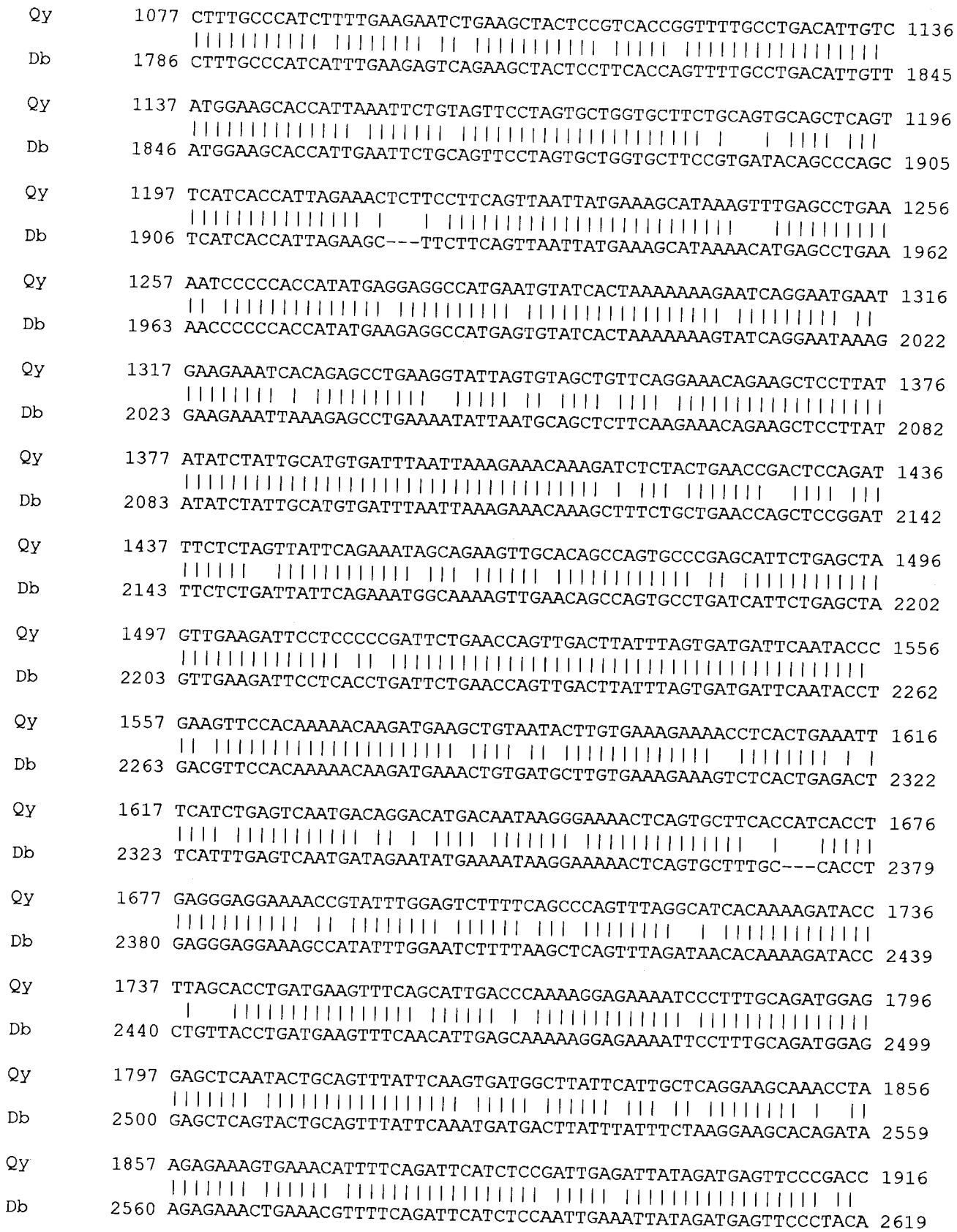

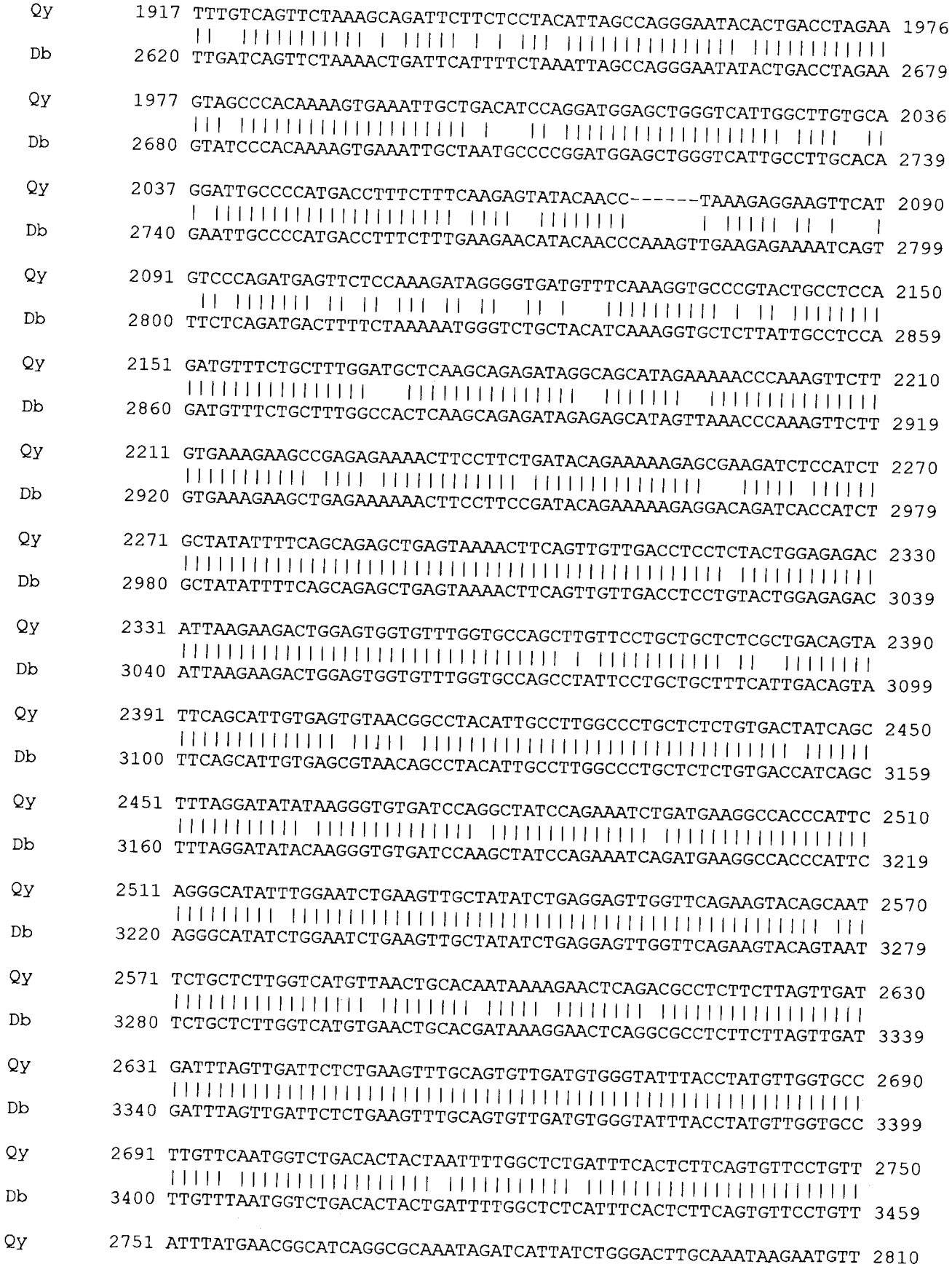

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Job time : 14434.6 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 10, 2004, 23:36:15 ; Search time 1342.11 Seconds
(without alignments)
12132.674 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
Sequence: 1 ctatctcctctctcagccgc.....ttaaaaaaaaaaaaaaaaaa 3833

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2649.8	69.1	4632	6	ABV94680	Abv94680 Human pan
4	2566.4	67.0	4698	7	ABX34563	Abx34563 Human mdd
5	2379.4	62.1	4053	4	AAS09453	Aas09453 Human cDN
6	2379.4	62.1	4053	8	ACC81048	Acc81048 Human Nog
7	2370.4	61.8	4093	3	AAA23454	Aaa23454 cDNA enco

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	10	2223.6	58.0	3579	6	ABK90134	Abk90134 DNA encod
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ALIGNMENTS

RESULT 1
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ID AAD01174 standard; cDNA; 3833 BP.
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AC AAD01174;
XX
DT 02-NOV-2000 (first entry)
XX
DE Bovine neurite growth inhibitor Nogo cDNA.
XX
KW Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; ss.
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OS Bos sp.
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PN WO200031235-A2.
XX
PD 02-JUN-2000.
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PF 05-NOV-1999; 99WO-US026160.
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PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 26; Fig 12; 122pp; English.
XX
CC The present sequence is a cDNA encoding bovine Nogo protein which is a
CC potent neural cell growth inhibitor and is free of all central nervous
CC system (CNS) myelin material with which it is natively associated. The
CC present sequence was obtained from bovine spinal cord white matter cDNA
CC library. Nogo proteins and fragments displaying neurite growth inhibitory
CC activity are used in the treatment of neoplastic disease of the CNS e.g.
CC glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve
CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
CC promote Nogo activity can be used to treat or prevent hyperproliferative
CC or benign dysproliferative disorders e.g. psoriasis and tissue
CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
CC inhibit production of Nogo protein to induce regeneration of neurons or
CC to promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However the specification does not include sequences for
CC these SEQ ID numbers
XX
SQ Sequence 3833 BP; 1235 A; 717 C; 818 G; 1063 T; 0 U; 0 Other;

Query Match 100.0%; Score 3833; DB 3; Length 3833;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3833; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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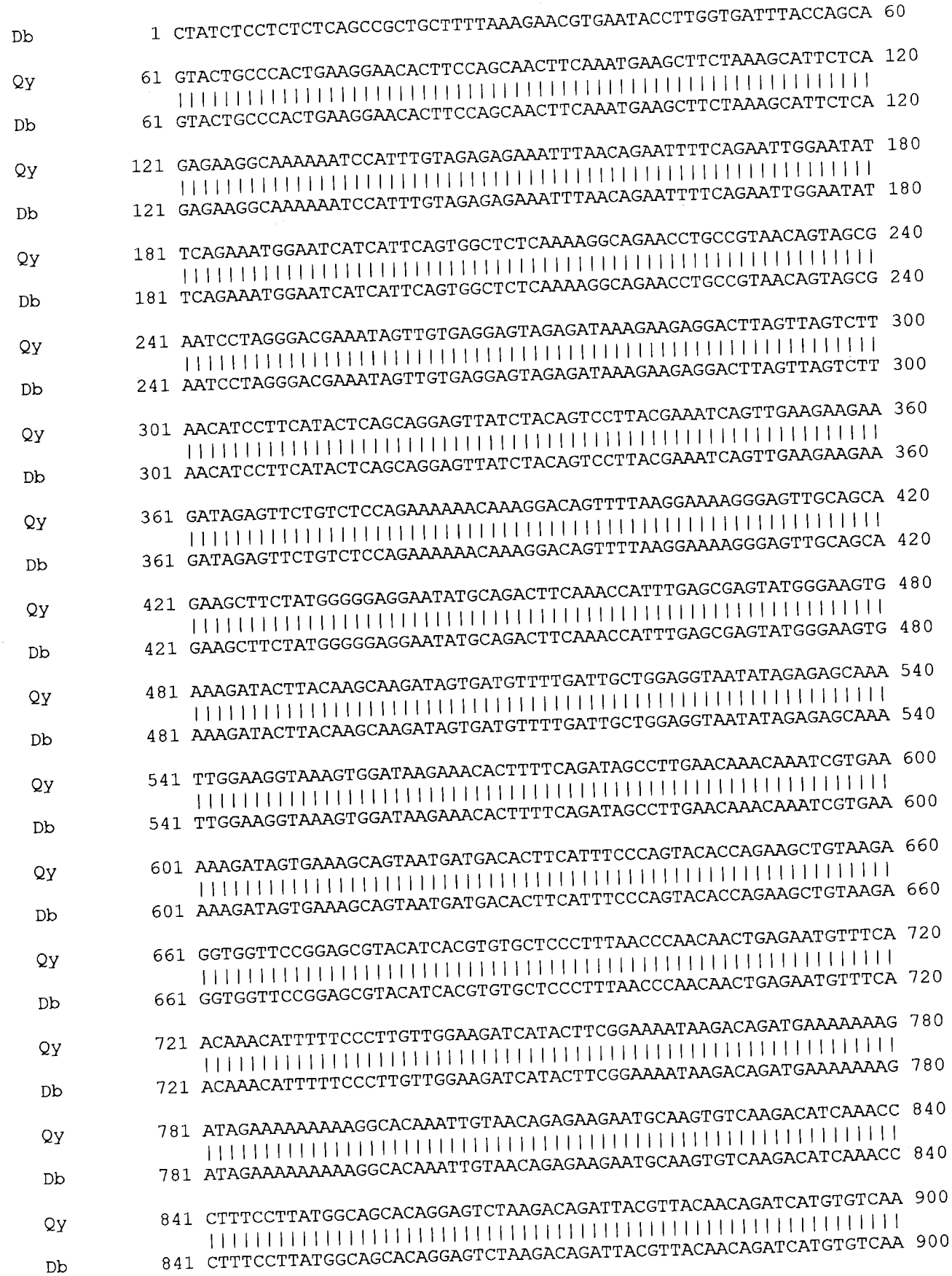

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Qy        961 AAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAAA 1020

Qy       1021 TGGACCTGGTTCAAACTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1081 GCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATGG 1140

Qy       1141 AAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCAT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCAT 1200

Qy       1201 CACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAATC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAATC 1260

Qy       1261 CCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAAGAATCAGGAATGAATGAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAAGAATCAGGAATGAATGAAG 1320

Qy       1321 AAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTATATAT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTATATAT 1380

Qy       1381 CTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCT 1440

Qy       1441 CTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTTG 1500

Qy       1501 AAGATTCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGATTCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAG 1560

Qy       1561 TTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCAT 1620
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Qy       1621 CTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAGG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAGG 1680

Qy       1681 GAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAG 1740
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Qy       1741 CACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAGGAGC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAGGAGC 1800

Qy       1801 TCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGAG 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGAG 1860

Qy       1861 AAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTTG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 AAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTTG 1920

Qy       1921 TCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTAG 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTAG 1980

Qy       1981 CCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCAGGAT 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCAGGAT 2040

Qy       2041 TGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCCAGATG 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 TGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCCAGATG 2100

Qy       2101 AGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCTG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCTG 2160

Qy       2161 CTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAAG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAAG 2220

Qy       2221 CCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTTT 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTTT 2280

Qy       2281 CAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGA 2340

Qy       2341 CTGGAGTGGTGTTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTG 2400
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Qy       2401 TGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATAT 2460
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Qy       2461 ATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCATATT 2520
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Qy       2521 TGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTG 2580

Qy       2581 GTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTG 2640
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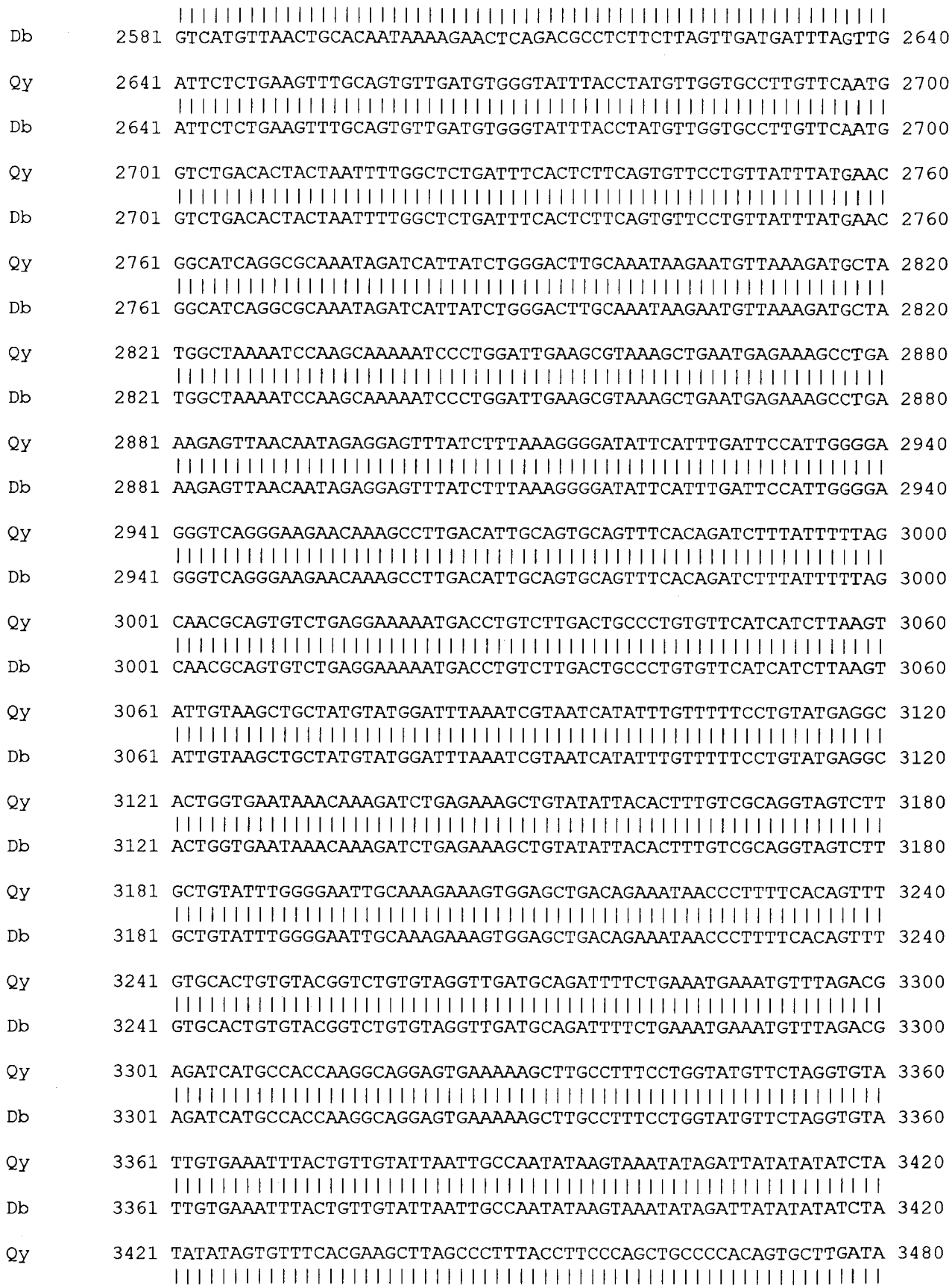

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Db       3421 TATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATA 3480

Qy       3481 CTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACT 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACT 3540

Qy       3541 TCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCA 3600
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Qy       3601 ACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCTGGACTGAAT 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 ACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCTGGACTGAAT 3660

Qy       3661 CTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAATATAAATGA 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAATATAAATGA 3720

Qy       3721 CGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAAC 3780
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Db       3721 CGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAAC 3780

Qy       3781 TGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAAA 3833
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 TGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAAA 3833
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RESULT 2
ABS70449
ID ABS70449 standard; cDNA; 4822 BP.
XX
AC ABS70449;
XX
DT 27-NOV-2002 (first entry)
XX
DE Human bone remodelling gene #106.
XX
KW Bone remodelling; osteoporosis; human; gene; ss.
XX
OS Homo sapiens.
XX
PN US6426186-B1.
XX
PD 30-JUL-2002.
XX
PF 18-JAN-2000; 2000US-00484970.
XX
PR 18-JAN-2000; 2000US-00484970.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Jones KA, Volkmuth W, Walker MG;
XX
DR WPI; 2002-673014/72.
XX
PT A combination of polynucleotides which are co-expressed with genes known
PT to be involved in bone remodeling and osteoporosis are useful in an array

PT for the diagnosis of bone remodeling and osteoporosis associated
PT disorders.
XX
PS Claim 1; Col 283-288; 206pp; English.
XX
CC The invention relates to a combination comprising a number of
CC substantially purified and isolated polynucleotides which are co-
CC expressed with genes known to be involved in bone remodelling and
CC osteoporosis. The invention is used to diagnose disorders associated with
CC bone remodelling or osteoporosis. ABS70344-ABS70512 represent human bone
CC remodelling genes of the invention
XX
SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;

Query Match 70.1%; Score 2687.8; DB 6; Length 4822;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 3333; Conservative 0; Mismatches 458; Indels 104; Gaps 27;

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Qy          1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
              || |||||||||||||||||| |||| ||||||| |||||||||||| |||| || ||
Db        964 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 1023

Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
              ||| | |||||||||||||||||| || || |   | ||||||||||||||   |||||
Db       1024 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 1083

Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
              |||||||||||| || | |  |||| ||| |||||||||| |||||||||| |||||
Db       1084 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1143

Qy        181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
              |||||||||| |||||| ||||||| ||||| ||| |||||| |||||||| ||||||
Db       1144 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1203

Qy        241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
              |||||||||| |||||| | |||| | || |||| |||||||| | |||||||||  |
Db       1204 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1263

Qy        301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
              |||||||||||| ||| || |||||| |||||| ||||| |||| ||| |||| ||
Db       1264 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1323

Qy        361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
              ||   |||| ||||| |||||||| |||| |||||||||| |||||| |||||||||
Db       1324 GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1380

Qy        421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
              |||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1440

Qy        481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
              ||||||| |   ||| |||||||||| | |||  |||||||||||| || ||||||||
Db       1441 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC 1497

Qy        541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
              |||||| |||||||||||| |||   ||| |||||||||||| ||||| ||||  |||
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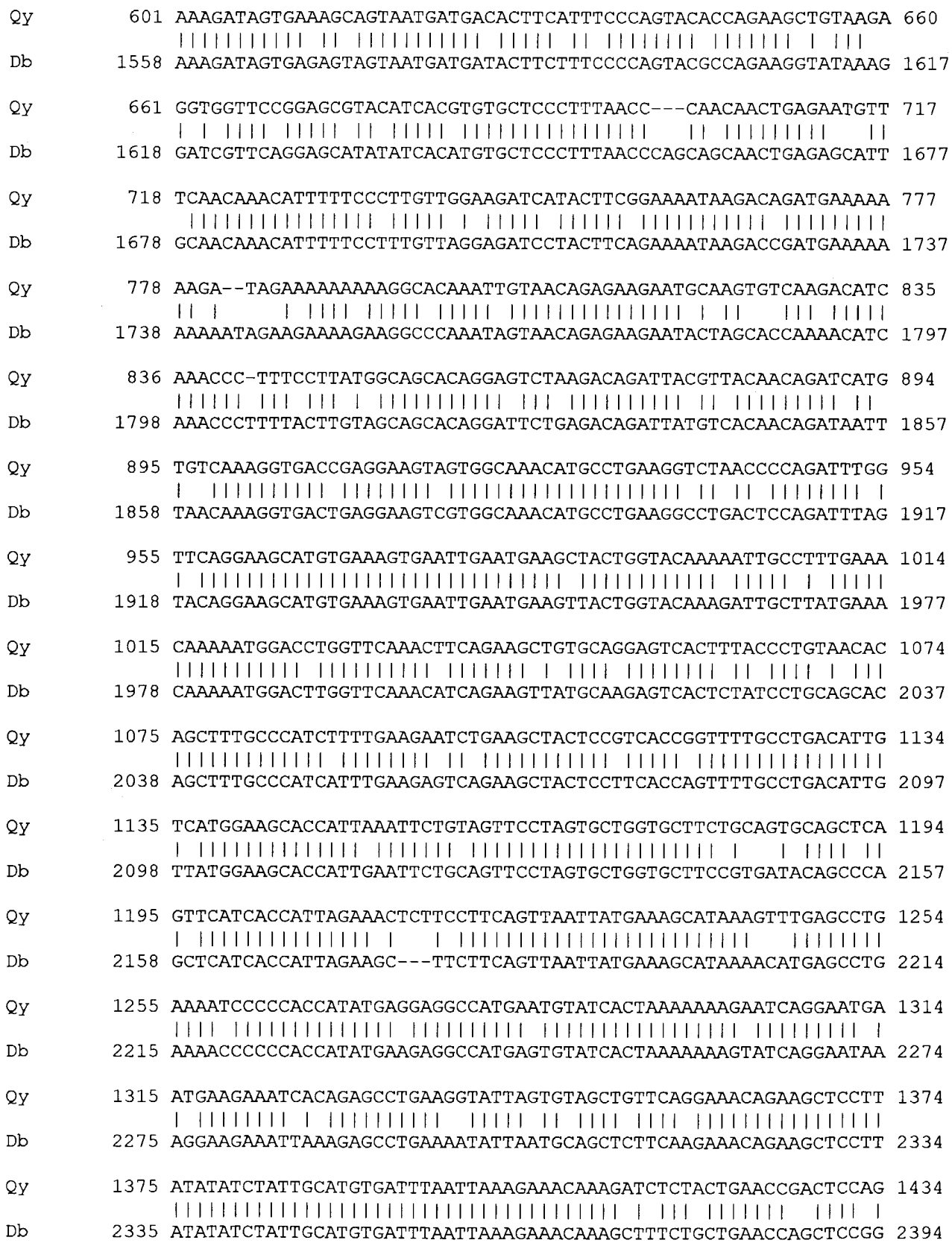

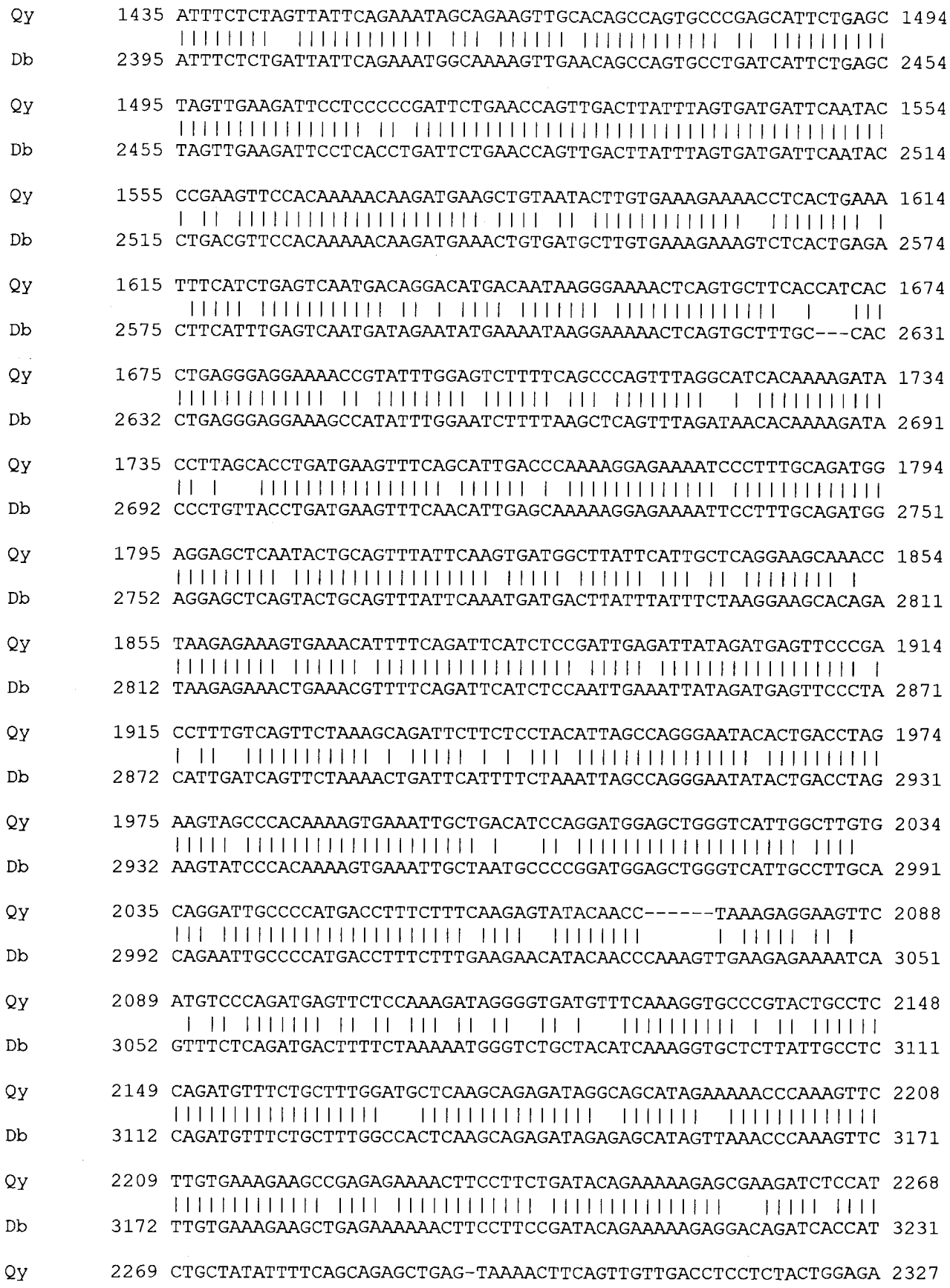

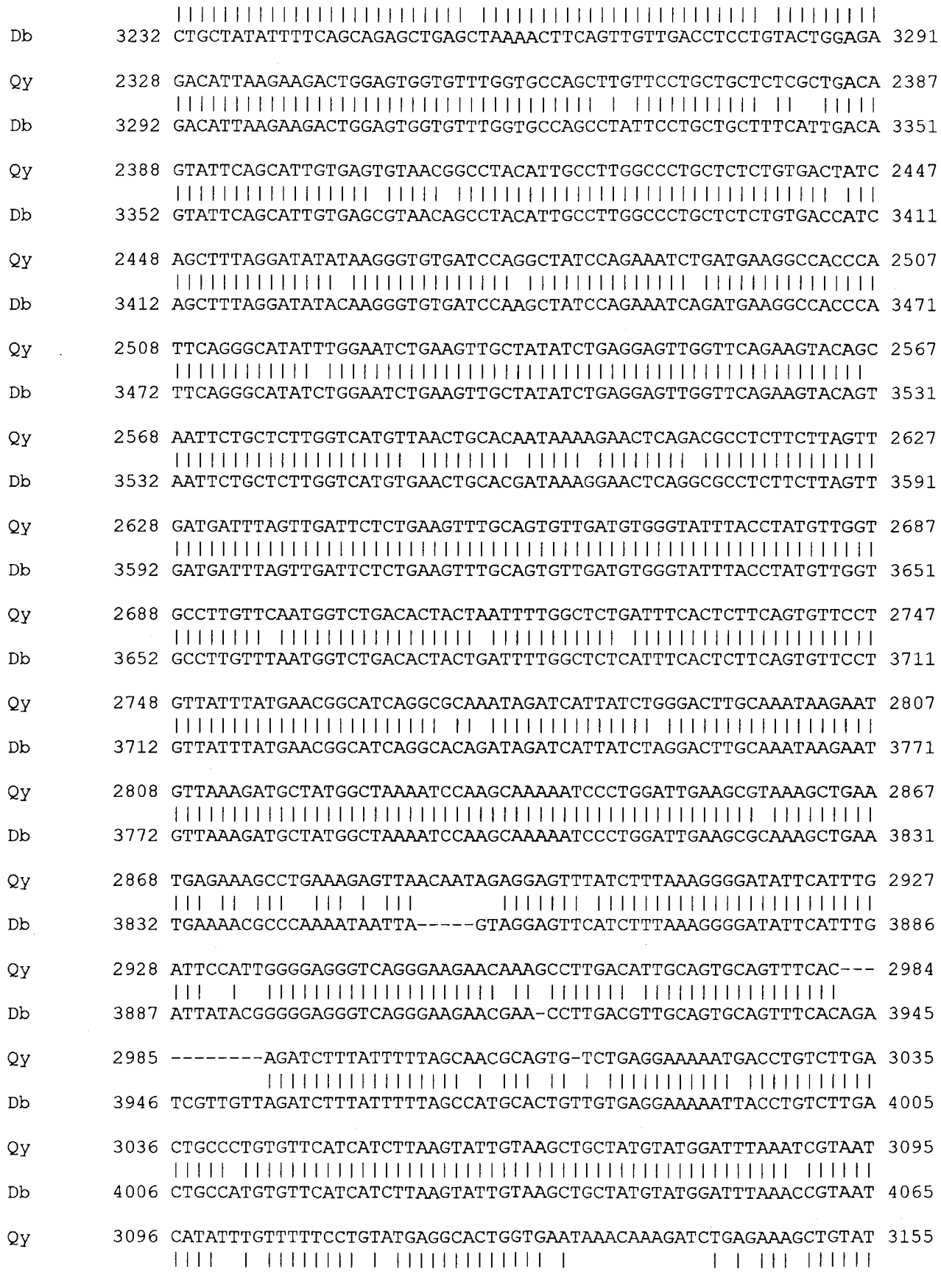

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Db       4066 CATA--TCTTTTTCCTATCTGAGGCACTGGTGGA-----------ATAAAAAACCTGTAT 4112

Qy       3156 ATTACACTTTGTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT 3214
              |||  ||||||| |||| ||||||||| | || ||||  | ||||| |||  ||||||||
Db       4113 ATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCT 4172

Qy       3215 --------GACAGAAATAACCCTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGT 3266
                     | | ||| ||  |  ||  |||||||||||||||||| |||| |||||| |
Db       4173 AGAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGAT 4232

Qy       3267 TGATGCAGATTTTCTGAAATGAAA----TGTTTAGACGAGATCATGCCACCAAGGCAGGA 3322
              ||||||||||||||||||||||||    |||||||||||||||| ||   || ||||||
Db       4233 TGATGCAGATTTTCTGAAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGA 4292

Qy       3323 GTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATT 3382
              ||| |||||||| |||| ||||||||||||||||||||||||  ||||||||| ||||
Db       4293 ATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATT 4351

Qy       3383 AATTGCCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTCACGAAGCTT 3442
              |||||||||||||||||||||||||||||||       |||||||||||| ||||||
Db       4352 AATTGCCAATATAAGTAAATATAGATTATATATG------TATAGTGTTTCACAAAGCTT 4405

Qy       3443 AGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT------TCTGTCATGGGTTT 3496
              || |||||||||| |||||  |||||||||||||||| |      || ||||| ||||
Db       4406 AGACCTTTACCTT-CCAGCCACCCCACAGTGCTTGATATTTCAGAGTCAGTCATTGGTTA 4464

Qy       3497 TATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCA 3556
              ||  |||||||| |||||||||||||||||    | |  || ||||||| |||||||||
Db       4465 TACATGTGTAGTTCCAAAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCA 4524

Qy       3557 TCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTG 3615
              |||||||||||||| |||   | ||||  || | ||||||||  |||||| || |||| ||
Db       4525 TCTGTTTTCAACATGAA---ATGCCACACACATAGAACTCCAACAACATCAATTTCATTG 4581

Qy       3616 CACAGACTTACTGTAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAA 3673
              |||||||| |||||||||||||||| ||||  || || |||||||||||||||||||||||
Db       4582 CACAGACTGACTGTAGTTAATTTTGTCACAGAATCTATGGACTGAATCTAATGCTTCCAA 4641

Qy       3674 AAA-------TGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT--------AAAT 3718
              |||       |||||||||||||||||||||||||| |||||| |||         ||||
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Qy       3719 GACGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGA 3778
              || ||||||||| |||||||||||||||| |||||||||||||||||||||||||||||
Db       4702 GAAGATTTATACCATTGTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGA 4761

Qy       3779 ACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAAA 3833
              |||||||||||||||||||||||||||||||||||||||    |  |   |||
Db       4762 ACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAANGNNANNAGNGAAA 4816
```

RESULT 3
ABV94680
ID   ABV94680 standard; cDNA; 4632 BP.
XX
AC   ABV94680;
XX

DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 53.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX
DR WPI; 2002-627435/67.
DR P-PSDB; ABP68600.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
PS Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;

Query Match 69.1%; Score 2649.8; DB 6; Length 4632;
Best Local Similarity 85.0%; Pred. No. 0;
Matches 3292; Conservative 0; Mismatches 442; Indels 137; Gaps 24;

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Qy          1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
              || |||||||||||||||||| |||| ||||||| |||||||||||| ||||  || ||
Db        853 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 912

Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
              ||| | |||||||||||||||||| || || |   | |||||||||||||   |||||
Db        913 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 972

Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
              |||||||||||| || | |  |||| ||| |||||||||| |||||||||| |||||
Db        973 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1032

Qy        181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
              |||||||||| |||||| ||||||| ||||| ||| |||||| ||||||||| ||||||
Db       1033 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1092

Qy        241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
              |||||||||| |||||| | |||| | || |||| |||||||| | |||||||||  |
Db       1093 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1152

Qy        301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
              |||||||||||| ||| || |||||| |||||  ||||  ||| |||| ||
Db       1153 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1212

Qy        361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
              ||   |||| ||||| |||||||| |||| |||||||||| |||||| |||||||||
Db       1213 GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1269

Qy        421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
              |||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1329

Qy        481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
              ||||||| |   ||| |||||||||| | |||  |||||||||||| || ||||||||
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Qy        541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
              |||||| |||||||||||| |||   ||| ||||||||||||| ||||| ||||  |||
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Qy        601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
              |||||||||| || |||||||||| ||||| || |||||||| ||||||| | |||
Db       1447 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG 1506

Qy        661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGTT 717
              | | |||| ||||| || ||||| ||||||||||||||||   || |||||||||   ||
Db       1507 GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1566

Qy        718 TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
               |||||||||||||||| ||||| | ||||| |||||| |||||||||| |||||||||
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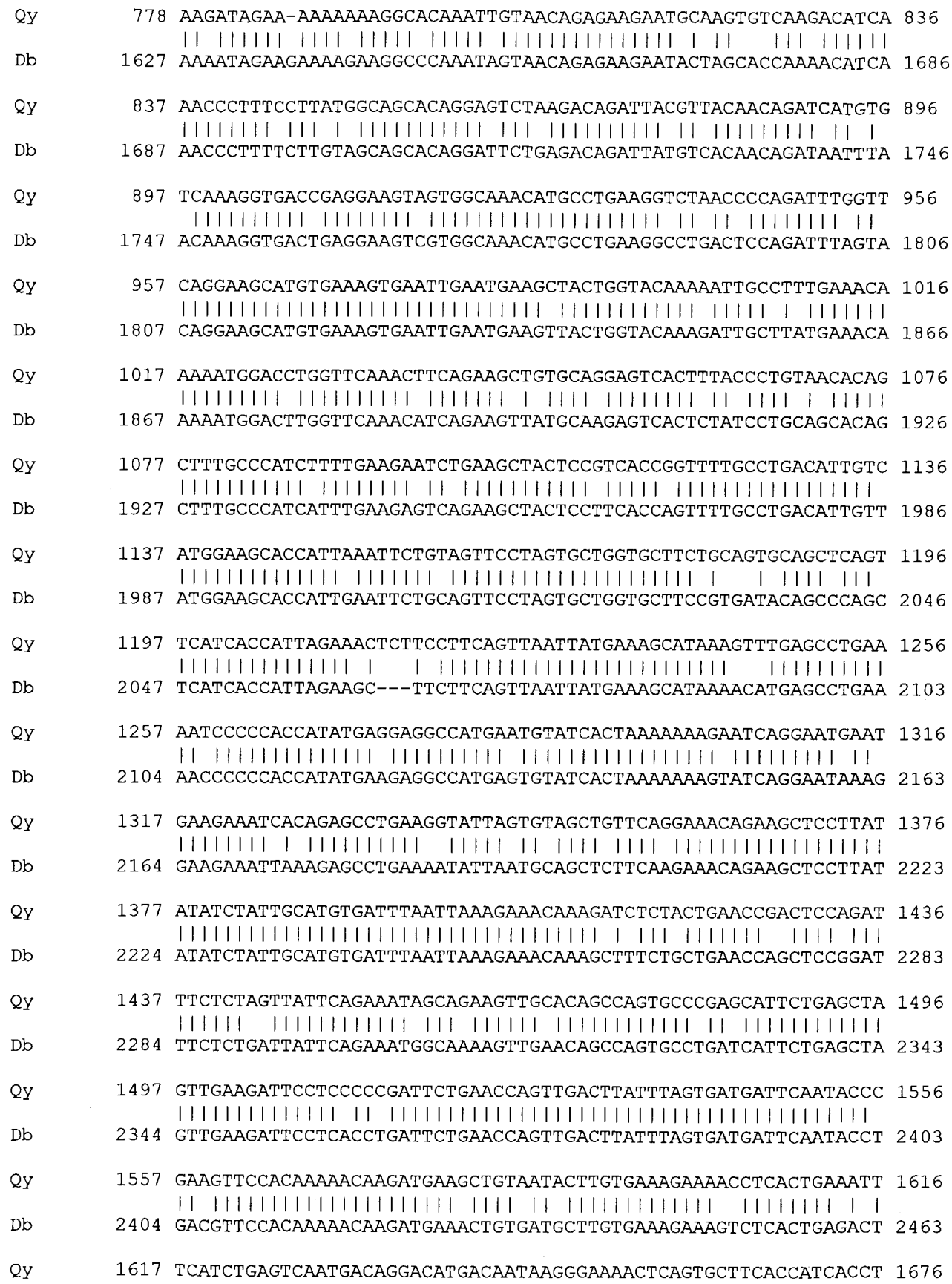

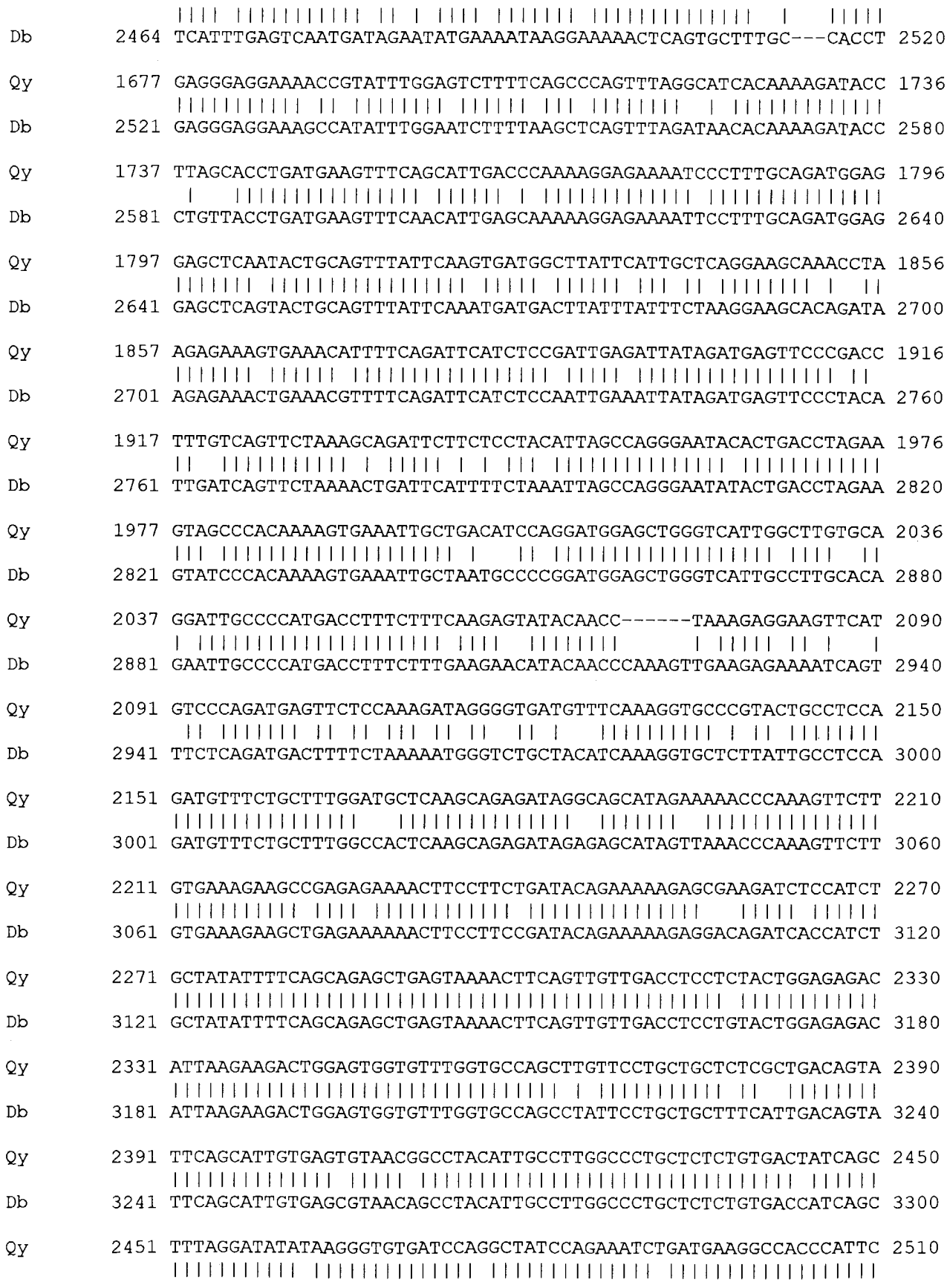

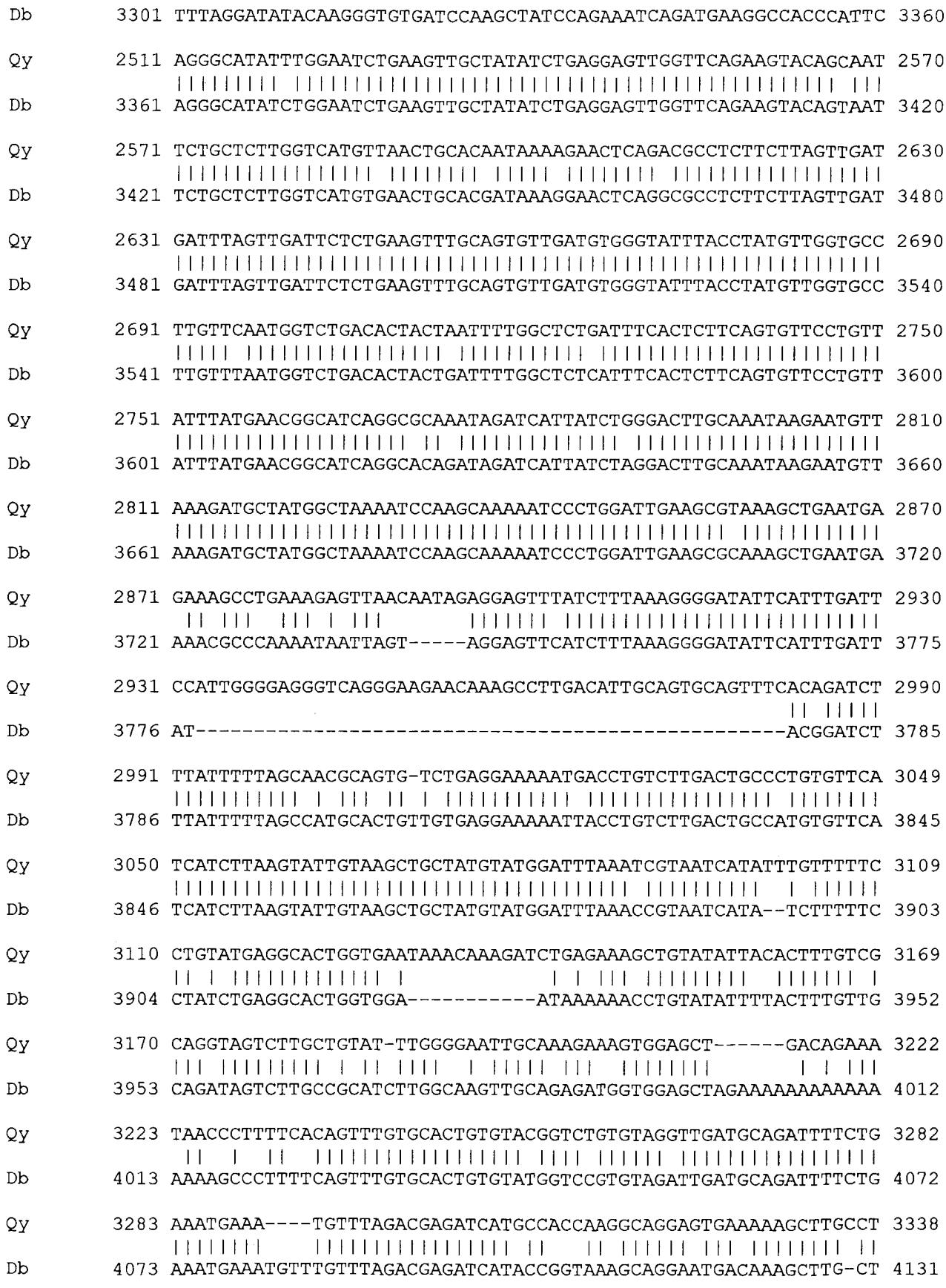

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Db       4132 TTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGT 4191

Qy       3399 AAATATAGATTATATATATCTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCC 3458
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Db       4192 AAATATAGATTATATATG------TATAGTGTTTCACAAAGCTTAGACCTTTACCTT-CC 4244

Qy       3459 AGCTGCCCCACAGTGCTTGATACT------TCTGTCATGGGTTTTATGTGTGTAGTCCCA 3512
              |||  |||||||||||||||| |      || ||||| |||| ||  |||||||| |||
Db       4245 AGCCACCCCACAGTGCTTGATATTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCA 4304

Qy       3513 AAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGA 3572
              ||||||||||||||    | |  || ||||||| |||||||||||||||||||| ||
Db       4305 AAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAACATGA 4364

Qy       3573 ACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTGCACAGACTTACTGTAG 3631
              |   | ||||  || | ||||||||  |||||| || |||| |||||||||| |||||||
Db       4365 A---ATGCCACACACATAGAACTCCAACAACATCAATTTCATTGCACAGACTGACTGTAG 4421

Qy       3632 TTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA-------TGTTTG 3682
              |||||||| ||||  || || |||||||||||||||||||||||||       ||||||
Db       4422 TTAATTTTGTCACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTTTG 4481

Qy       3683 CAAATATCAAACATTGTTATGTAAGAAAATAT--------AAATGACGATTTATACAATT 3734
              |||||||||||||||||||| |||||| |||        |||||| ||||||||| |||
Db       4482 CAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACCATT 4541

Qy       3735 GTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGT 3794
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Db       4542 GTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGT 4601

Qy       3795 ATCAATAAAGCTTATAGACTTAAAAAAAAAA 3825
              |||||||||||||||||||||||||||||
Db       4602 ATCAATAAAGCTTATAGACTTAAAAAAAAAA 4632
```

RESULT 4
ABX34563
ID ABX34563 standard; cDNA; 4698 BP.
XX
AC ABX34563;
XX
DT 13-FEB-2003 (first entry)
XX
DE Human mddt cDNA SEQ ID 124.
XX
KW MDDT; human; disease detection and treatment molecule polypeptide;
KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW gene therapy; protein replacement therapy; cell proliferative disorder;
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
KW psoriasis; hepatitis; gene; ss.
XX

OS Homo sapiens.
XX
PN WO200279449-A2.
XX
PD 10-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-US009944.
XX
PR 28-MAR-2001; 2001US-0279619P.
PR 29-MAR-2001; 2001US-0280067P.
PR 29-MAR-2001; 2001US-0280068P.
PR 16-MAY-2001; 2001US-0291280P.
PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-058431/05.
DR P-PSDB; ABU11573.
XX
PT New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis.
XX
PS Claim 1; SEQ ID NO 124; 339pp + Sequence Listing; English.
XX
CC This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in
CC ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 4698 BP; 1410 A; 1028 C; 1022 G; 1238 T; 0 U; 0 Other;

Query Match 67.0%; Score 2566.4; DB 7; Length 4698;

Best Local Similarity 84.7%; Pred. No. 0;
Matches 3221; Conservative 0; Mismatches 441; Indels 140; Gaps 25;

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Qy          1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
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Db        856 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 915

Qy         61 GTACTGCCCACTGAAGGAACACTTCCAG-CAACTTCAAATGAAGCTTCTAAAGCATTCTC 119
              ||| | |||||||||||||||||||| ||  || |   | |||||||||||||   ||||
Db        916 GTATTACCCACTGAAGGAACACTTCAAGAAAAATGTCAGTGAAGCTTCTAAAGAGGTCTC 975

Qy        120 AGAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATA 179
              |||||||||||||| || | |  |||| ||| |||||||||| |||||||||| |||||
Db        976 AGAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATA 1035

Qy        180 TTCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGC 239
              |||||||||| |||||| ||||||| ||||| ||| |||||| ||||||||| ||||||
Db       1036 CTCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGC 1095

Qy        240 GAATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCT 299
              |||||||||| |||||| | |||| | || |||| |||||||| | |||||||||
Db       1096 AAATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAA 1155

Qy        300 TAACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGA 359
              |||||||||||||| ||| || |||||| |||||| ||||| |||| ||| |||| ||
Db       1156 TAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGA 1215

Qy        360 AGATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGC 419
              ||   |||| ||||| |||||||| |||| |||||||||| |||||| |||||||||
Db       1216 TGA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGT 1272

Qy        420 AGAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGT 479
              |||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 GGAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGT 1332

Qy        480 GAAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAA 539
              |||||||| |   ||| |||||||||| | |||  |||||||||||| || ||||||||
Db       1333 GAAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAA 1389

Qy        540 ATTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGA 599
              |||||| |||||||||||| |||   ||| |||||||||||| ||||| ||||  ||
Db       1390 CTTGGAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGA 1449

Qy        600 AAAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAG 659
              |||||||||||| || |||||||||| ||||| || |||||||| ||||||| | |||
Db       1450 AAAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAA 1509

Qy        660 AGGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGT 716
              | | |||| ||||| || ||||| ||||||||||||||||   || |||||||||   |
Db       1510 GGATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCAT 1569

Qy        717 TTCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAA 776
              | |||||||||||||||| ||||| | ||||| |||||| |||||||||| ||||||||
Db       1570 TGCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAA 1629

Qy        777 AAAGATAGAA-AAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATC 835
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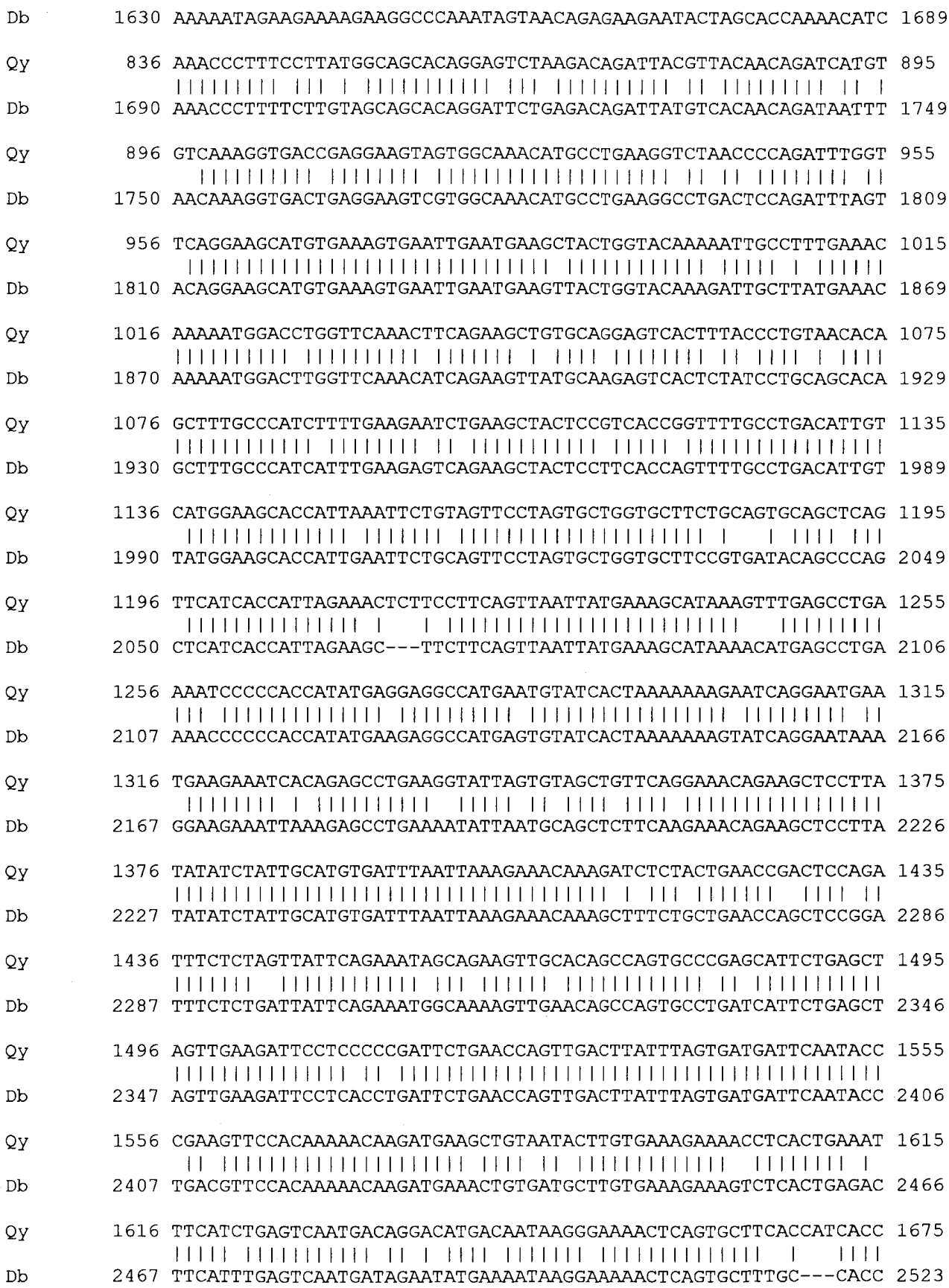

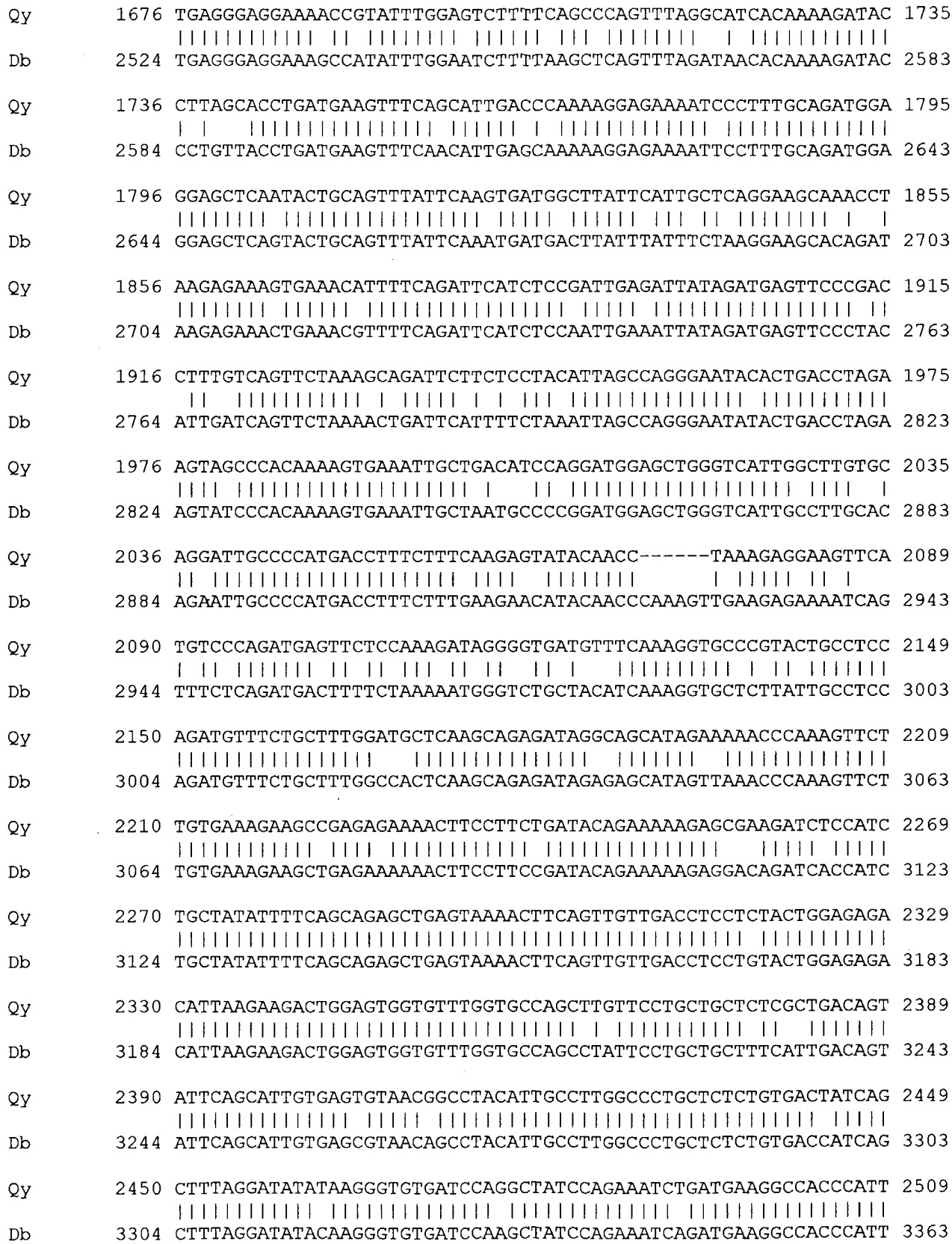

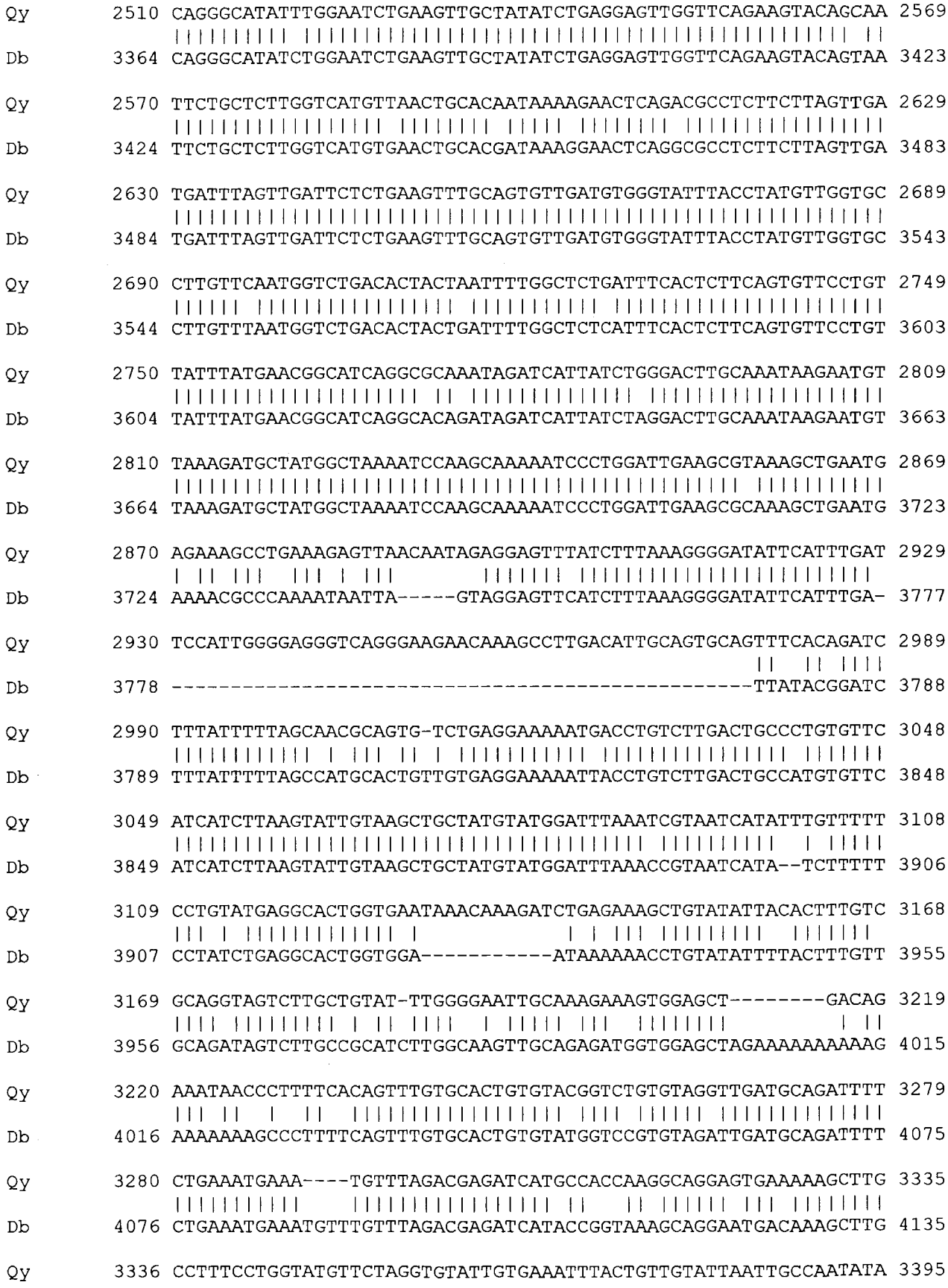

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Qy       3396 AGTAAATATAGATTATATATATCTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTT 3455
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Db       4195 AGTAAATATAGATTATA------TATGTATAGTGTTTCACAAAGCTTAGACCTTTACCTT 4248

Qy       3456 CCCAGCTGCCCCACAGTGCTTGATACT------TCTGTCATGGGTTTTATGTGTGTAGTC 3509
               |||||  |||||||||||||||| |      || ||||| |||| ||  |||||||
Db       4249 -CCAGCCACCCCACAGTGCTTGATATTTCAGAGTCAGTCATTGGTTATACATGTGTAGTT 4307

Qy       3510 CCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACA 3569
              ||||||||||||||||    | |  || ||||||| ||||||||||||||||||||
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Qy       3570 CGAACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTGCACAGACTTACTG 3628
               |||   | ||||  || | ||||||||  |||||| || |||| |||||||||| ||||
Db       4368 TGAA---ATGCCACACACATAGAACTCCAACAACATCAATTTCATTGCACAGACTGACTG 4424

Qy       3629 TAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA-------TGT 3679
              |||||||||| ||||  || || ||||||||||||||||||||||||       |||
Db       4425 TAGTTAATTTTGTCACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGT 4484

Qy       3680 TTGCAAATATCAAACATTGTTATGTAAGAAAATAT--------AAATGACGATTTATACA 3731
              |||||||||||||||||||||| |||||| |||        |||||| |||||||||
Db       4485 TTGCAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACC 4544

Qy       3732 ATTGTGGTTTAAGCTGTATTGA 3753
              |||||||||||||||||| |||
Db       4545 ATTGTGGTTTAAGCTGTACTGA 4566
```

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RESULT 5
AAS09453
ID   AAS09453 standard; cDNA; 4053 BP.
XX
AC   AAS09453;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human cDNA encoding the Nogo protein.
XX
KW   Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;
KW   cranial trauma; cerebral trauma; spinal cord injury; stroke;
KW   demyelinating disease; multiple sclerosis; monophasis demyelination;
KW   encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;
KW   Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;
KW   Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;
KW   Canavan's disease; metachromatic leukodystrophy; viral infection;
KW   Krabbe's disease; AB020693; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             135. .3713
FT                   /*tag=  a
FT                   /product= "Nogo protein"
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XX
PN WO200151520-A2.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001041.
XX
PR 12-JAN-2000; 2000US-0175707P.
PR 26-MAY-2000; 2000US-0207366P.
PR 29-SEP-2000; 2000US-0236378P.
XX
PA (UYYA) UNIV YALE.
XX
PI Strittmatter SM;
XX
DR WPI; 2001-442138/47.
DR P-PSDB; AAU09453.
XX
PT Novel Nogo receptor protein useful for identifying modulator of Nogo
PT protein or Nogo receptor protein, which is useful for treating central
PT nervous system disorders.
XX
PS Example 1; Page 95-100; 109pp; English.
XX
CC The sequence (Genbank accession number AB0202693) encodes the human Nogo
CC protein, a 250kDa myelin-associated axon growth inhibitor. The invention
CC relates to the use of the nogo receptor, nogo protein, their nucleic
CC acids, vectors expressing them and antibodies against them, to isolate
CC agents which block nogo receptor mediated axonal growth. The agent is
CC useful for treating a central nervous system disorder which is a result
CC of cranial or cerebral trauma, spinal cord injury, stroke or a
CC demyelinating disease selected from multiple sclerosis, monophasis
CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,
CC panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis,
CC adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration,
CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy,
CC viral infection and Krabbe's disease
XX
SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;

Query Match 62.1%; Score 2379.4; DB 4; Length 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

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Qy          1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
              || ||||||||||||||||||| |||| ||||||| |||||||||||| ||||  || ||
Db        846 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 905

Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
              ||| | |||||||||||||||||| || || |   | ||||||||||||||   |||||
Db        906 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965

Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
              |||||||||||| || | |  |||| ||| |||||||||| |||||||||| |||||
Db        966 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1025

Qy        181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
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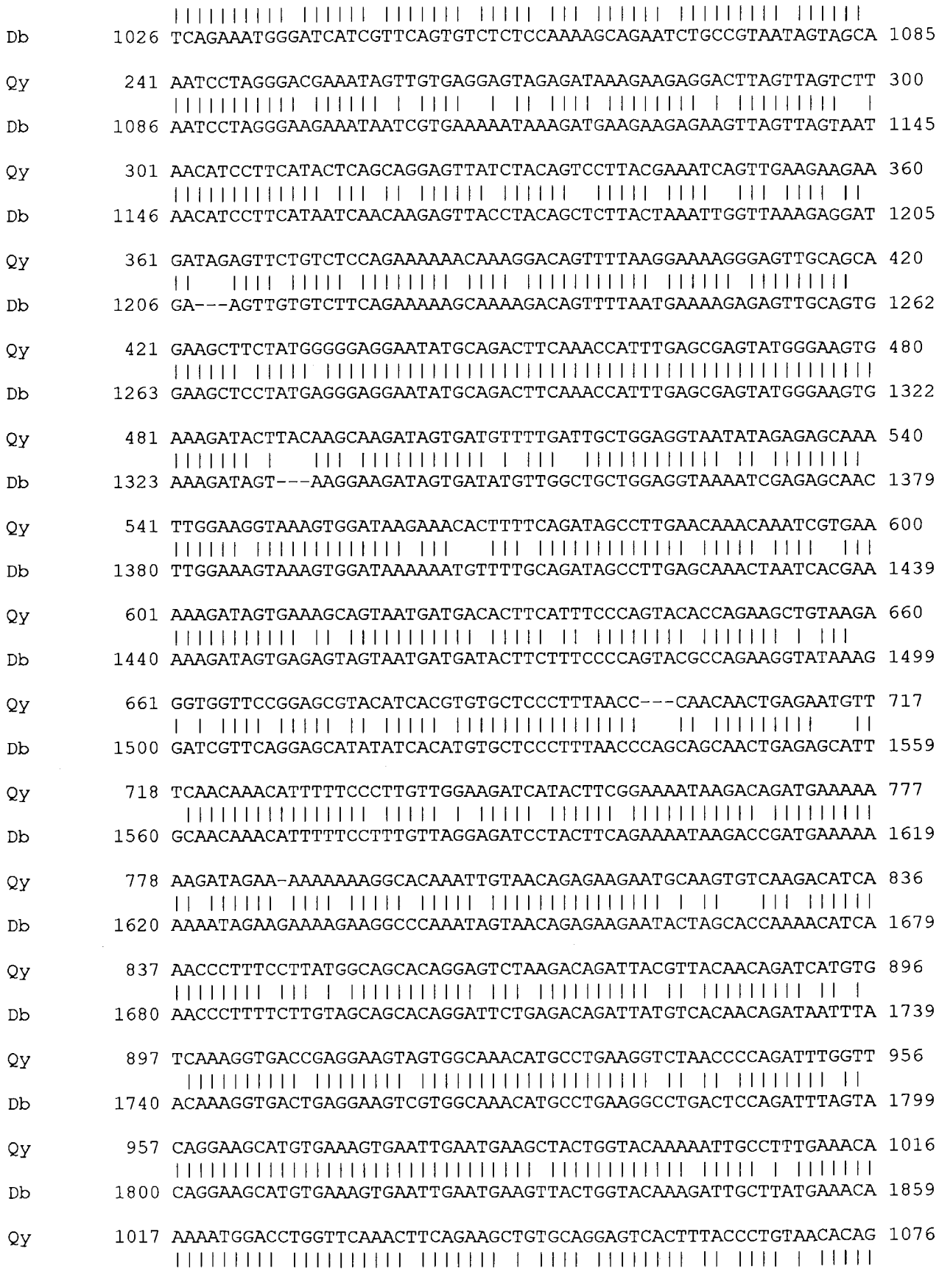

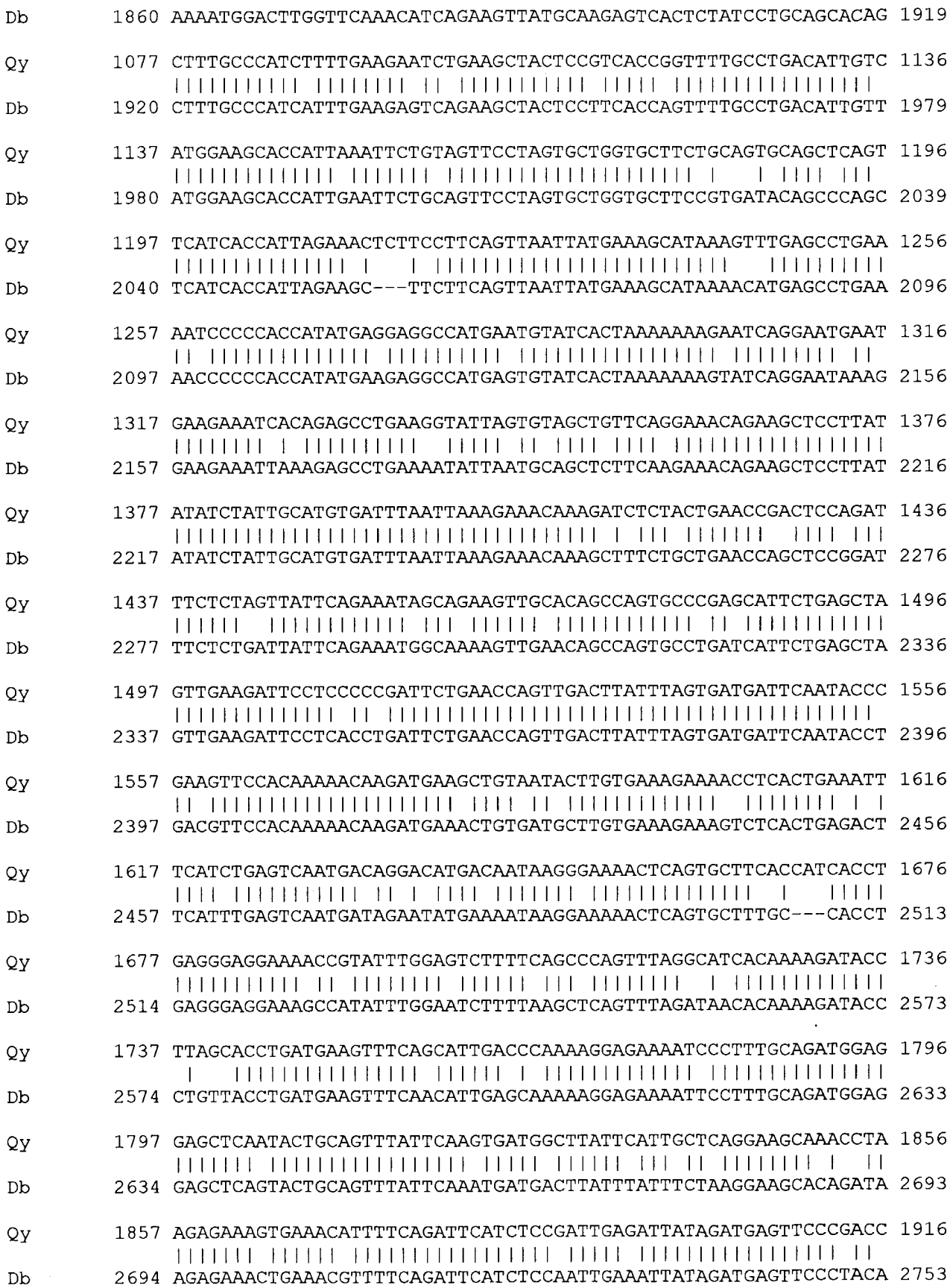

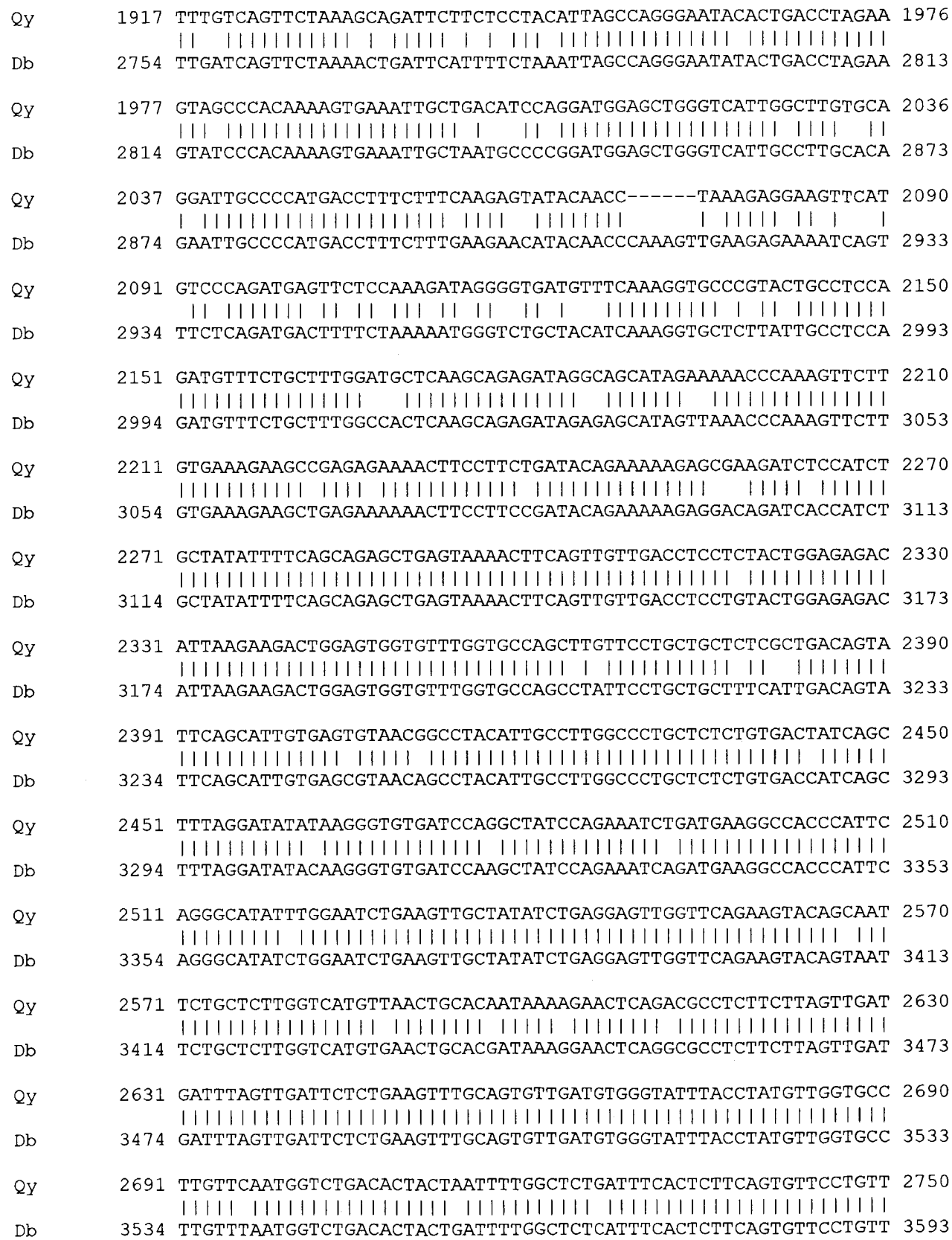

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Db       3594 ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT 3653

Qy       2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       3654 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3713

Qy       2871 GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT 2930
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Db       3714 AAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT 3768

Qy       2931 CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC------ 2984
               |  |||||||||||||||||||| || ||||||| ||||||||||||||||
Db       3769 ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG 3827

Qy       2985 -----AGATCTTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG 3038
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Db       3828 TTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTG 3887

Qy       3039 CCCTGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT 3098
             || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       3888 CCATGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT 3947

Qy       3099 ATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATT 3158
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Db       3948 A--TCTTTTTCCTATCTGAGGCACTGGTGGA----------ATAAAAAACCTGTATATT 3994

Qy       3159 ACACTTTGTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT 3214
               ||||||| |||| ||||||||| | || ||||  | ||||| |||  ||||||||
Db       3995 TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCT 4051
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RESULT 6
ACC81048
ID   ACC81048 standard; cDNA; 4053 BP.
XX
AC   ACC81048;
XX
DT   22-JUL-2003  (first entry)
XX
DE   Human NogoA gene.
XX
KW   Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy;
KW   axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
KW   cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
KW   demyelinating disease; multiple sclerosis; monophasic demyelination;
KW   encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             135. .3713
FT                   /*tag=  a
FT                   /product= "Human NogoA"
XX
```

PN WO2003031462-A2.
XX
PD 17-APR-2003.
XX
PF 04-OCT-2002; 2002WO-US032007.
XX
PR 06-OCT-2001; 2001US-00972599.
XX
PA (UYYA) UNIV YALE.
XX
PI Strittmatter SM;
XX
DR WPI; 2003-393433/37.
DR P-PSDB; ABR59667.
XX
PT New human Nogo receptor polypeptides and nucleic acids, useful for
PT decreasing inhibition of axonal growth by a central nervous system
PT neuron, or in treating central nervous system disease, disorder or
PT injury, e.g. spinal cord injury.
XX
PS Disclosure; Page 126-131; 148pp; English.
XX
CC The invention relates to a novel nucleic acid encoding a polypeptide
CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
CC human Nogo receptor (NgR) NTLRRCT domain), or residues 27-309 of P1 with
CC 1-20 conservative amino acid substitutions, and less than a complete CTS
CC domain, provided that a partial CTS domain, if present, consists of no
CC more than the first 39 consecutive residues. The nucleic acid of the
CC invention has neuroprotective activity. The polynucleotide may have a use
CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
CC axonal growth by a central nervous system (CNS) neuron. The NgR
CC polypeptide or an agent inhibits the binding of Nogo to NgR or NgR-
CC dependent signal transduction in the central nervous system neuron may be
CC used in treating central nervous system disease, disorder or injury, e.g.
CC spinal cord injury. Expression of an NgR protein may be associated with
CC inhibition of axonal regeneration following cranial, cerebral or spinal
CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
CC monophasic demyelination, encephalomyelitis, multifocal
CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
CC sequence is used in the exemplification of the invention
XX
SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;

Query Match 62.1%; Score 2379.4; DB 8; Length 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

```
Qy          1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
              || |||||||||||||||||| |||| ||||||| |||||||||||| ||||  || ||
Db        846 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 905

Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
              ||| | |||||||||||||||||| || || |   | ||||||||||||||   |||||
Db        906 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965

Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
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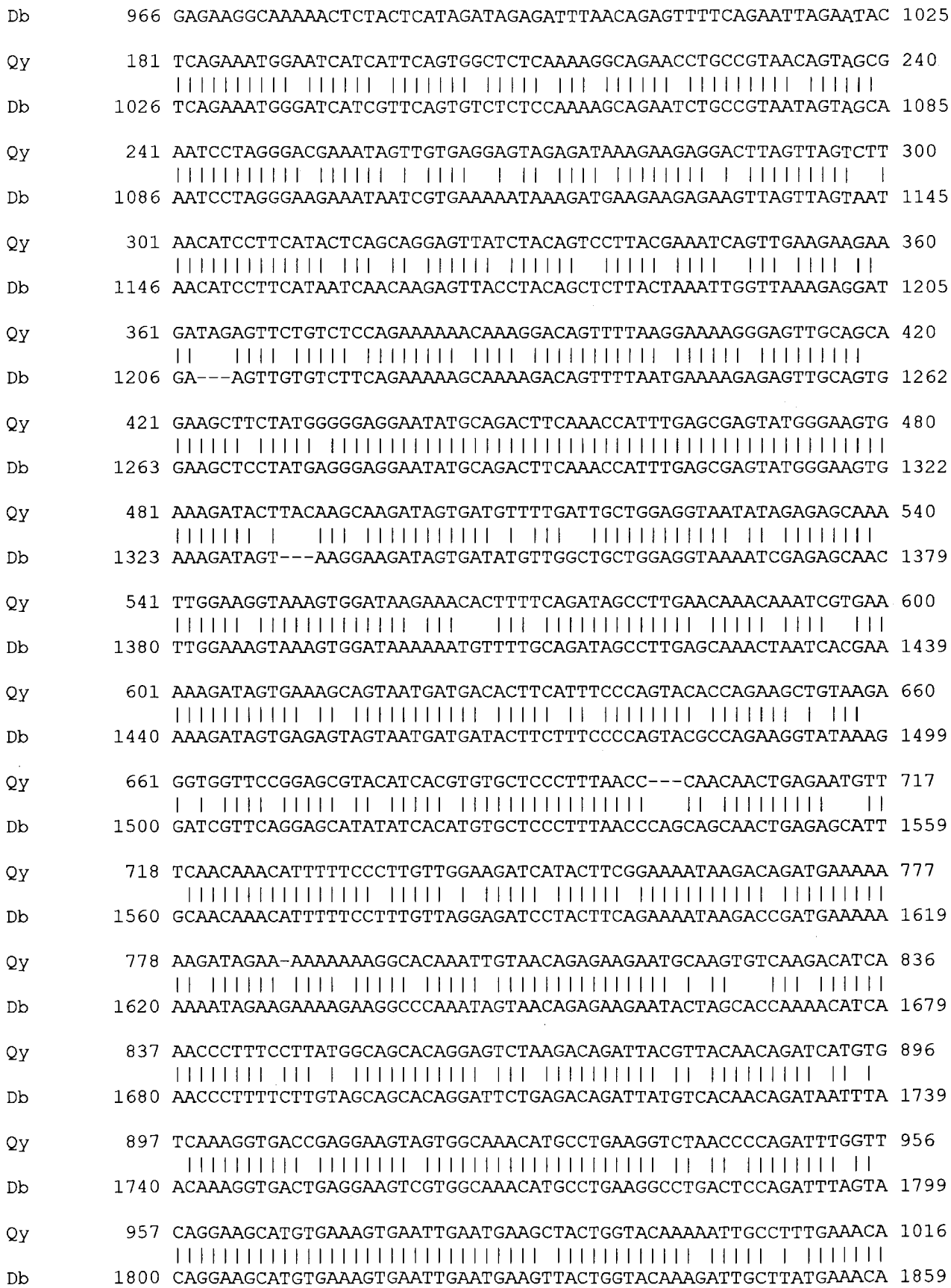

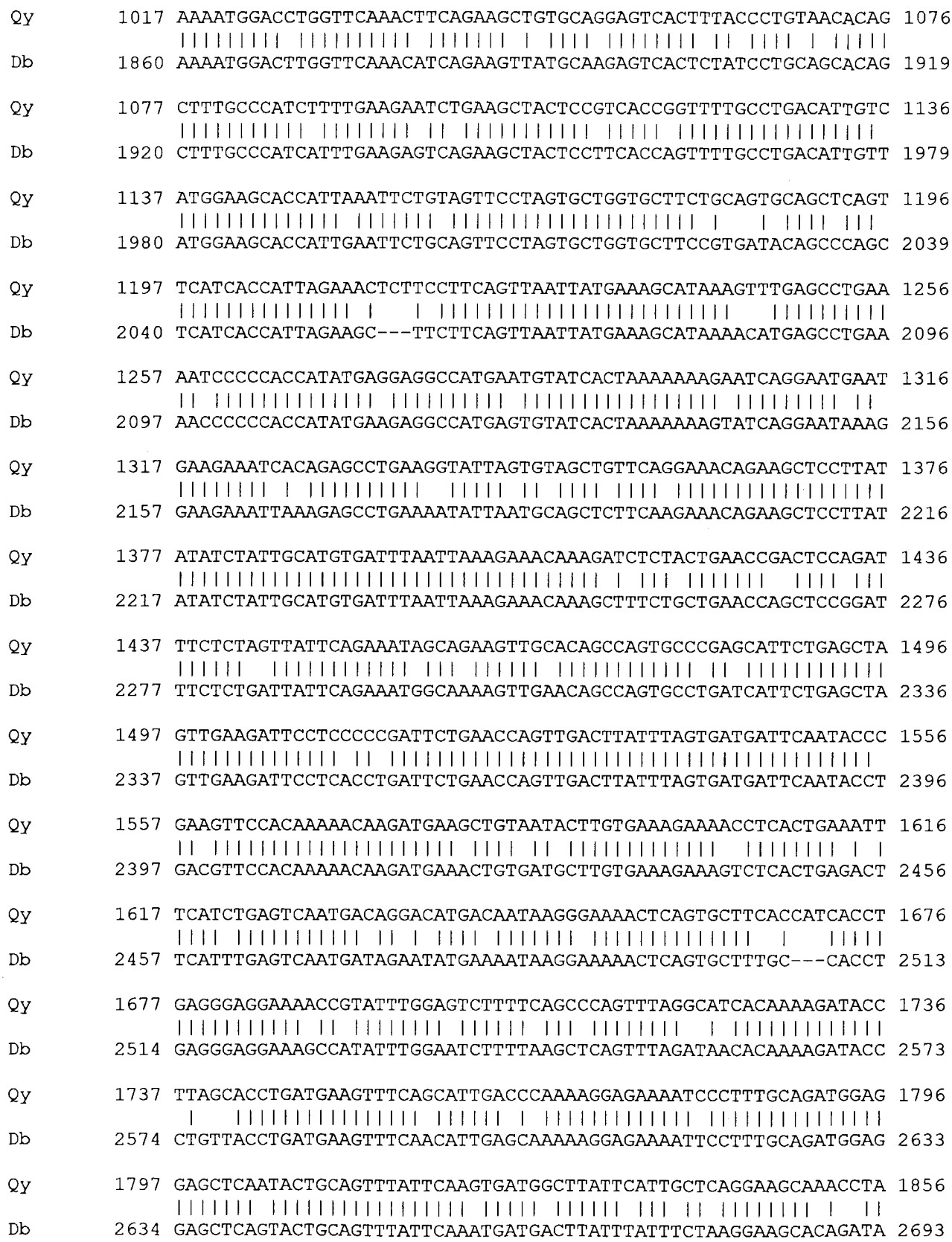

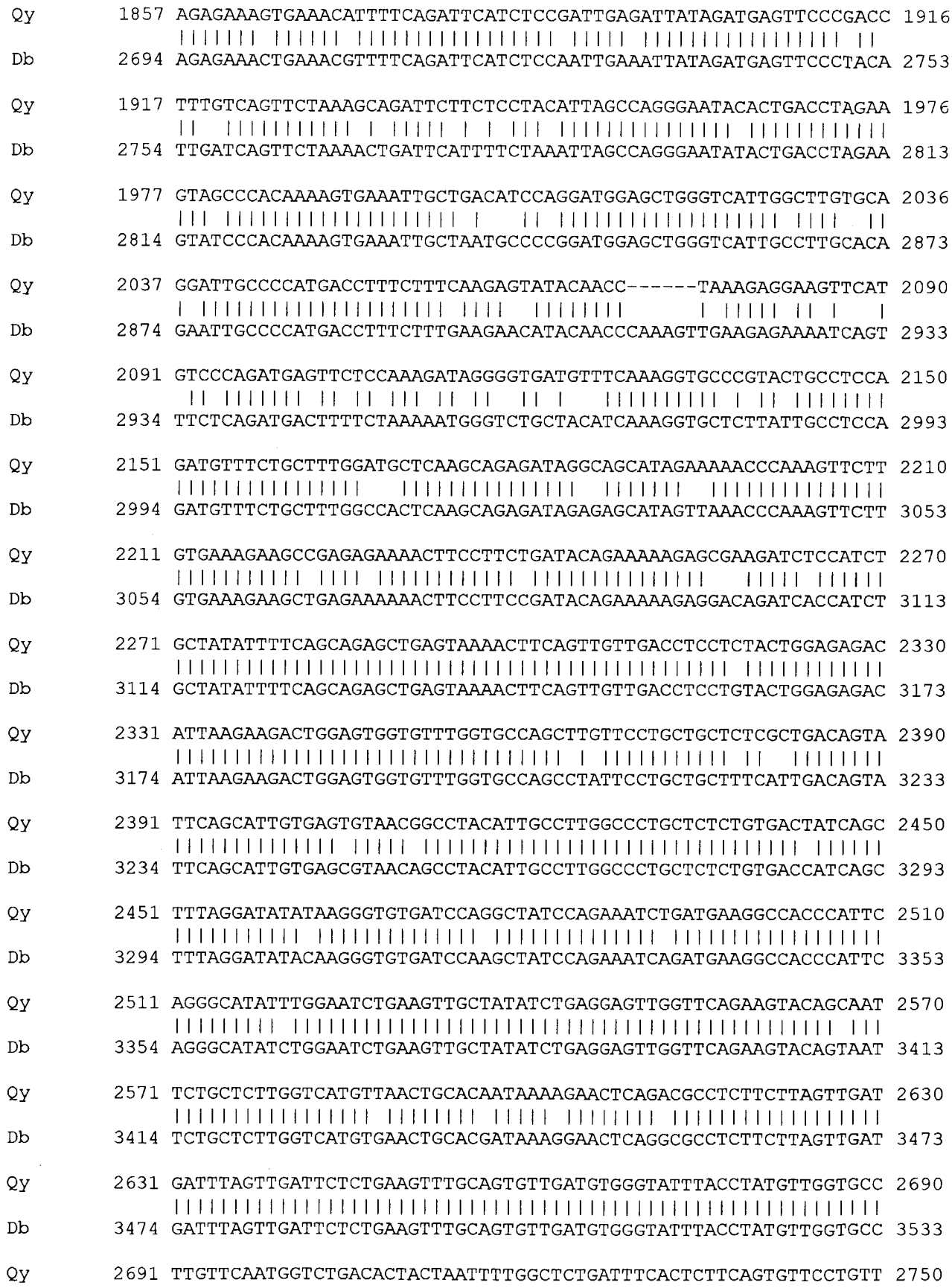

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Qy       2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
                ||||||||||||||||||| || |||||||||||||| ||||||||||||||||||||
Db       3594 ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT 3653

Qy       2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
                |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       3654 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3713

Qy       2871 GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT 2930
                || |||  ||| | |||       ||||||| ||||||||||||||||||||||||||
Db       3714 AAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT 3768

Qy       2931 CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC------ 2984
                |  |||||||||||||||||| || ||||||| ||||||||||||||||
Db       3769 ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG 3827

Qy       2985 -----AGATCTTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG 3038
                    |||||||||||||||| | ||| || | |||||||||| ||||||||||||||
Db       3828 TTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTG 3887

Qy       3039 CCCTGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT 3098
                || ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       3888 CCATGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT 3947

Qy       3099 ATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATT 3158
                |  | |||||||| | |||||||||||||| |            | | ||| |||||||||
Db       3948 A--TCTTTTTCCTATCTGAGGCACTGGTGGA-----------ATAAAAAACCTGTATATT 3994

Qy       3159 ACACTTTGTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT 3214
                |||||||  |||| |||||||||  | ||  ||||  | |||||  |||  ||||||||
Db       3995 TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCT 4051
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RESULT 7
AAA23454
ID AAA23454 standard; cDNA; 4093 BP.
XX
AC AAA23454;
XX
DT 19-JUN-2000 (first entry)
XX
DE cDNA encoding human secreted protein vb22_1, SEQ ID NO:63.
XX
KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   152. .1006
FT   /*tag= b
FT   /product= "Clone vb22_1 ORF2"

FT CDS 1048. .3729
FT /*tag= a
FT /product= "Human secreted protein vb22_1"
XX
PN WO200011015-A1.
XX
PD 02-MAR-2000.
XX
PF 24-AUG-1999; 99WO-US019351.
XX
PR 24-AUG-1998; 98US-0097638P.
PR 24-AUG-1998; 98US-0097659P.
PR 09-SEP-1998; 98US-0099618P.
PR 28-SEP-1998; 98US-0102092P.
PR 25-NOV-1998; 98US-0109978P.
PR 23-DEC-1998; 98US-0113645P.
PR 23-DEC-1998; 98US-0113646P.
PR 23-AUG-1999; 99US-00379246.
XX
PA (ALPH-) ALPHAGENE INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-224657/19.
DR P-PSDB; AAY95012, AAY95030.
XX
PT New secreted or transmembrane proteins and polynucleotides encoding them,
PT useful for treating neurodegenerative disorders, autoimmune diseases and
PT cancer.
XX
PS Claim 72; Page 321-322; 357pp; English.
XX
CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins
CC of the invention include those that are thought to be only partially
CC secreted, i.e., transmembrane proteins. The proteins of the invention may
CC exhibit one or more activities selected from the following: cytokine
CC activity; cell proliferation; differentiation; immune modulation;
CC haematopoiesis regulation; tissue growth activity; activin/inhibin
CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC activity; anti-inflammatory activity; and tumour inhibition activity. The
CC proteins may be administered to patients as vaccines, and the nucleotides
CC may be used as part of a gene therapy regime. Diseases or conditions that
CC may be treated using the proteins or nucleotides of the invention include
CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular
CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;
CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;
CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and
CC allergic reactions such as asthma and anaemia. They may also be used for
CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal
CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease
CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin
CC activity may additionally be useful as contraceptives. Nucleic acid
CC sequences of the invention may be used in chromosome mapping, and as a
CC source of diagnostic primers and probes. The present sequence represents
CC cDNA encoding one of the 40 proteins of the invention
XX

SQ Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 U; 0 Other;

Query Match 61.8%; Score 2370.4; DB 3; Length 4093;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 2807; Conservative 0; Mismatches 386; Indels 55; Gaps 15;

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Qy          1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
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Db        863 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 922

Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
              ||| | |||||||||||||||||| || || |   | ||||||||||||   |||||
Db        923 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 982

Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
              |||||||| |||| || | |  |||| ||| |||||||||| |||||||||| |||||
Db        983 GAGAAGGC-AAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1041

Qy        181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
              |||||||||| |||||| ||||||| ||||| ||| |||||| |||||||| ||||||
Db       1042 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1101

Qy        241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
              |||||||||| |||||| | |||| | || |||| |||||||| | |||||||||  |
Db       1102 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1161

Qy        301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
              |||||||||||| ||| || |||||| ||||||  ||||| ||||  ||| |||| ||
Db       1162 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1221

Qy        361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
              ||   |||| ||||| |||||||| |||| |||||||||| |||||| |||||||||
Db       1222 GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1278

Qy        421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
              |||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1338

Qy        481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
              ||||||| |   ||| |||||||||| | |||  |||||||||||| || ||||||||
Db       1339 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC 1395

Qy        541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
              |||||| |||||||||||| |||   ||| |||||||||||| ||||| ||||  |||
Db       1396 TTGGAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAA 1455

Qy        601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
              |||||||||| || |||||||||| ||||| || |||||||| ||||||| | |||
Db       1456 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG 1515

Qy        661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGTT 717
              | | |||| ||||| || ||||| ||||||||||||||||   || |||||||||   ||
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Qy        718 TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
               |||||||||||||||| ||||| | ||||| |||||| |||||||||| |||||||||
Db       1576 GCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA 1635
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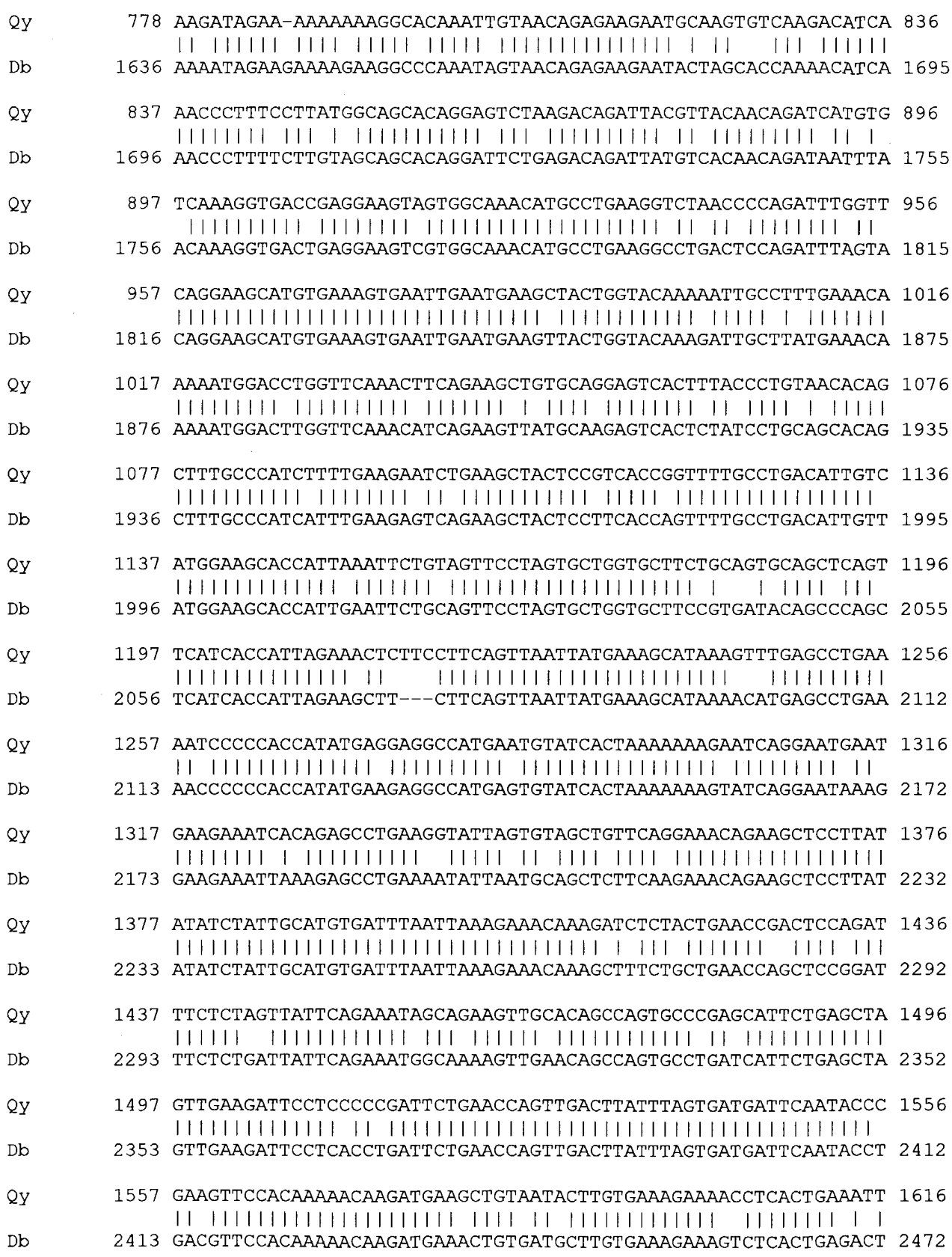

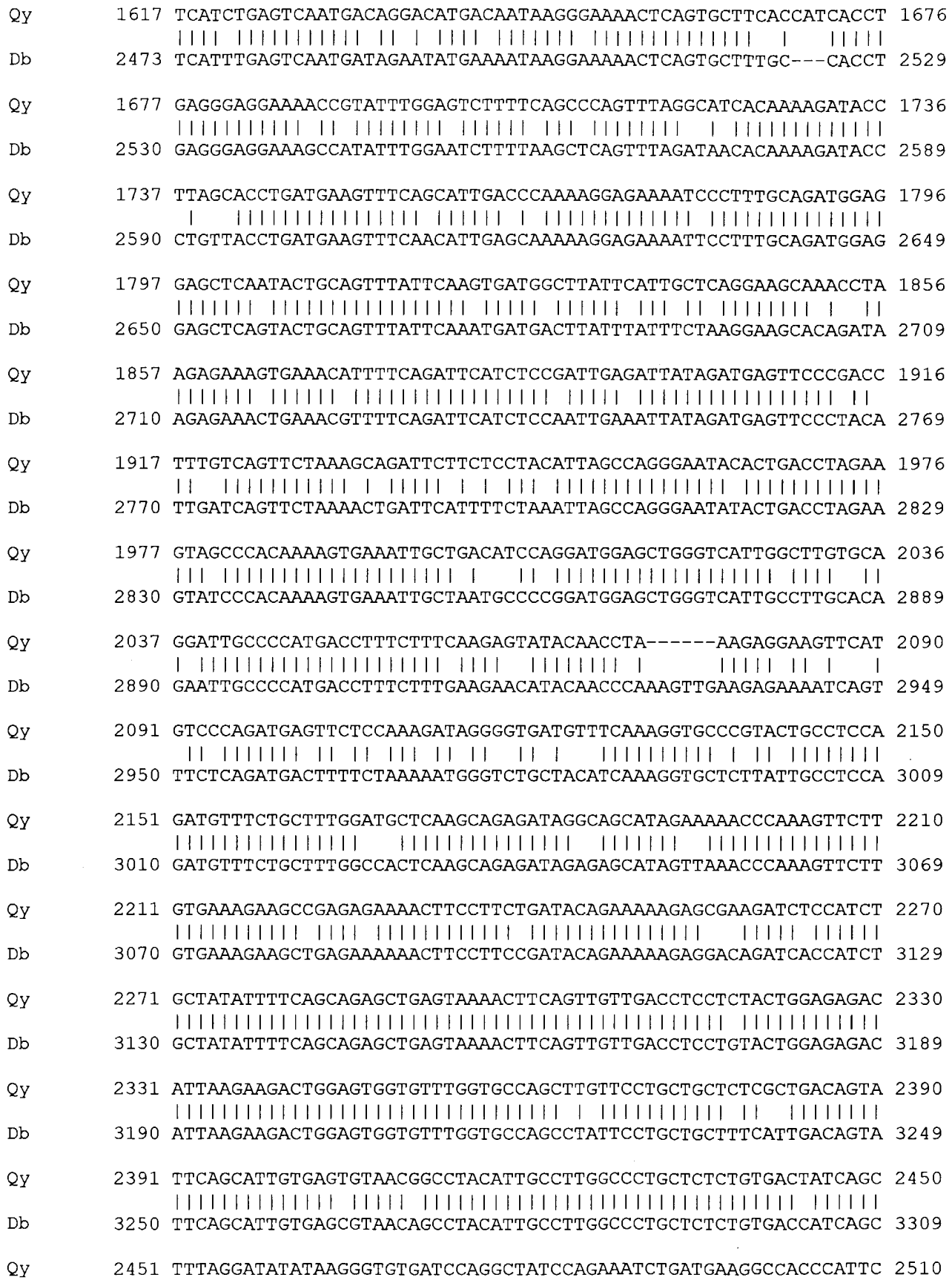

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Db       3370 AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT 3429

Qy       2571 TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT 2630

Db       3430 TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT 3489

Qy       2631 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 2690

Db       3490 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 3549

Qy       2691 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT 2750

Db       3550 TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT 3609

Qy       2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810

Db       3610 ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT 3669

Qy       2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870

Db       3670 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3729

Qy       2871 GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT 2930

Db       3730 AAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT 3784

Qy       2931 CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC------ 2984

Db       3785 ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG 3843

Qy       2985 -----AGATCTTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG 3038

Db       3844 TTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTG 3903

Qy       3039 CCCTGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT 3098

Db       3904 CCATGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT 3963

Qy       3099 ATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATT 3158

Db       3964 A--TCTTTTTCCTATCTGAGGCACTGGTGGA-----------ATAAAAAACCTGTATATT 4010

Qy       3159 ACACTTTGTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCTGAC 3217

Db       4011 TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGA 4070

Qy       3218 AGAAATAA 3225

Db       4071 AAAAAAAA 4078
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RESULT 8

AAZ56886
ID AAZ56886 standard; DNA; 3579 BP.
XX
AC AAZ56886;
XX
DT 25-APR-2000 (first entry)
XX
DE Human MAGI polypeptide encoding DNA.
XX
KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;
KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
KW psychiatric disorder; developmental disorder; inflammatory disorder;
KW stroke; cytostatic; cerebroprotective; neuroprotective; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .3579
FT   /*tag= a
FT   /product= "MAGI polypeptide"
XX
PN WO200005364-A1.
XX
PD 03-FEB-2000.
XX
PF 21-JUL-1999; 99WO-GB002360.
XX
PR 22-JUL-1998; 98GB-00016024.
PR 19-JUL-1999; 99GB-00016898.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Michalovich D, Prinjha RK;
XX
DR WPI; 2000-182693/16.
DR P-PSDB; AAY56967.
XX
PT Novel polypeptides related to neuroendocrine-specific proteins and
PT polynucleotides useful for diagnosis of various diseases and for
PT treatment of cancer and neurological disorders.
XX
PS Claim 5; Page 19-20; 35pp; English.
XX
CC The invention relates to human MAGI protein, which is similar to
CC neuroendocrine-specific protein. The MAGI protein can be expressed by
CC standard recombinant methodology. The MAGI polypeptides, polynucleotides
CC and antibodies are useful for treating diseases, including neuropathies,
CC spinal injury, neuronal degeneration, neuromuscular disorders,
CC psychiatric disorders and developmental disorders, cancer, stroke and
CC inflammatory disorders. The polynucleoitde is also useful for chromosome
CC localization and for tissue expression studies. The present sequence
CC represents a DNA encoding the human MAGI protein
XX
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

  Query Match   58.0%; Score 2223.6; DB 3; Length 3579;
  Best Local Similarity   87.5%; Pred. No. 0;

Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy          1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
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Db        712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
              ||| | |||||||||||||||||| || || |   | |||||||||||||   |||||
Db        772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
              |||||||||||| || | |  |||| ||| |||||||||| |||||||||| |||||
Db        832 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 891

Qy        181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
              |||||||||| |||||| ||||||| ||||| ||| |||||| |||||||| ||||||
Db        892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 951

Qy        241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
              |||||||||| |||||| | |||| | || |||| |||||||| | |||||||||  |
Db        952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy        301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
              |||||||||||| ||| || |||||| |||||| ||||| |||| ||| |||| ||
Db       1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy        361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
              ||   |||| ||||| |||||||| |||| |||||||||| |||||| |||||||||
Db       1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1128

Qy        421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
              |||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

Qy        481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
              ||||||| |   ||| |||||||||| | |||  |||||||||| || ||||||||
Db       1189 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC 1245

Qy        541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
              |||||| |||||||||||| |||   ||| |||||||||||| ||||| ||||  |||
Db       1246 TTGGAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAA 1305

Qy        601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
              |||||||||| || |||||||||| ||||| || |||||||| ||||||| | |||.
Db       1306 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG 1365

Qy        661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGTT 717
              | | || | ||||| || ||||| ||||||||||||||||   || |||||||||   ||
Db       1366 GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1425

Qy        718 TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
               ||||||||||||||| ||||| | ||||| |||||| |||||||||| |||||||||
Db       1426 GCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA 1485

Qy        778 AAGATAGAA-AAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA 836
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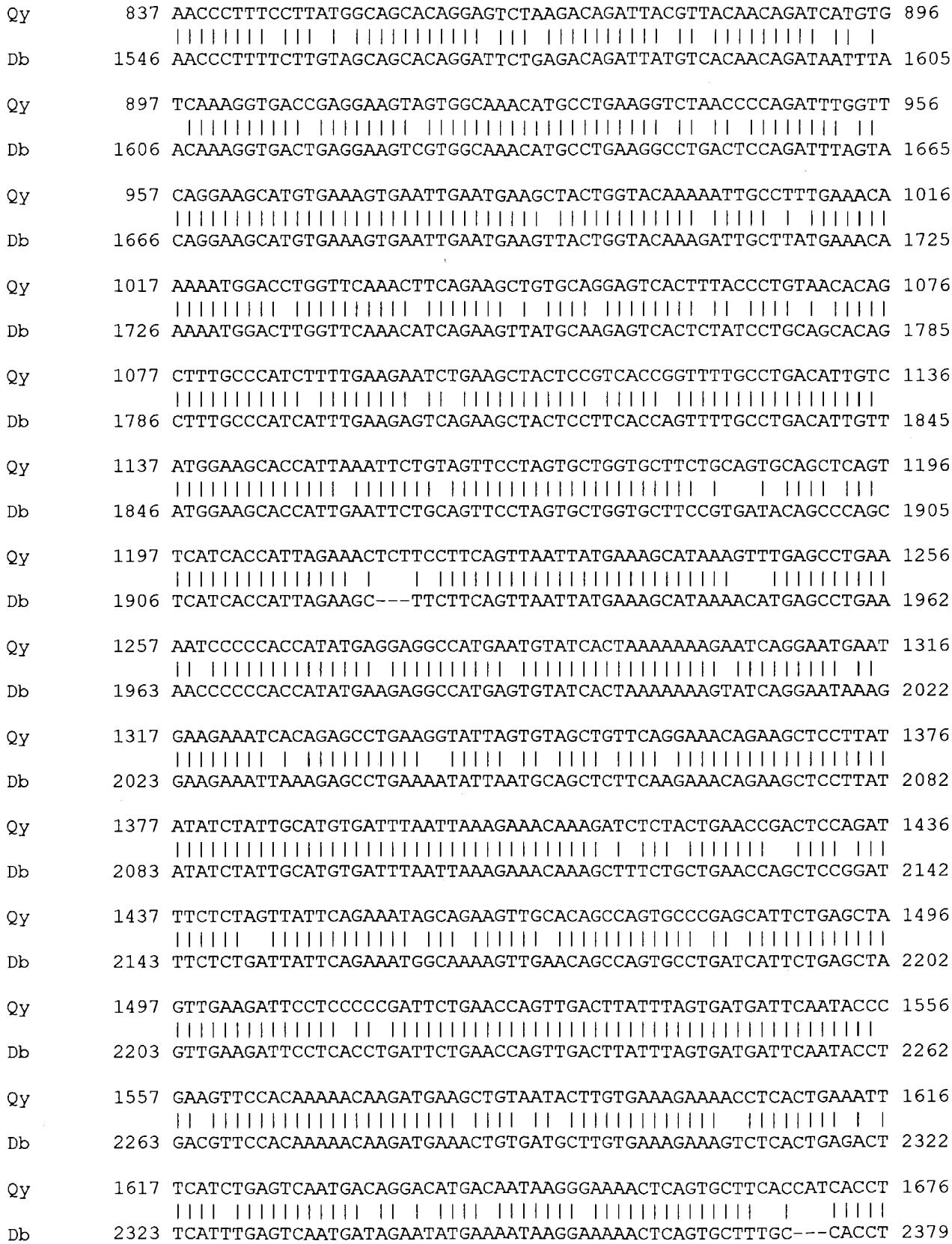
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Db 1546 AACCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA 1605
Qy 897 TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGTT 956
Db 1606 ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA 1665
Qy 957 CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA 1016
Db 1666 CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA 1725
Qy 1017 AAAATGGACCTGGTTCAAACTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG 1076
Db 1726 AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG 1785
Qy 1077 CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC 1136
Db 1786 CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT 1845
Qy 1137 ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT 1196
Db 1846 ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC 1905
Qy 1197 TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA 1256
Db 1906 TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA 1962
Qy 1257 AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAAAGAATCAGGAATGAAT 1316
Db 1963 AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAAGTATCAGGAATAAAG 2022
Qy 1317 GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTAT 1376
Db 2023 GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT 2082
Qy 1377 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT 1436
Db 2083 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT 2142
Qy 1437 TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA 1496
Db 2143 TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA 2202
Qy 1497 GTTGAAGATTCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC 1556
Db 2203 GTTGAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT 2262
Qy 1557 GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT 1616
Db 2263 GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT 2322
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Db 2323 TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGC---CACCT 2379

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Qy       1677 GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC 1736
             |||||||||||  ||  ||||||||  ||||||  |||  ||||||||   |  ||||||||||||
Db       2380 GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC 2439

Qy       1737 TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG 1796
              |   ||||||||||||||||  ||||||  |  ||||||||||||  ||||||||||||||||
Db       2440 CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG 2499

Qy       1797 GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA 1856
             |||||||  ||||||||||||||||||  |||||  ||||||  |||  ||  ||||||||  |  ||
Db       2500 GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA 2559

Qy       1857 AGAGAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC 1916
             |||||||  ||||||  ||||||||||||||||||  |||||  ||||||||||||||||||  ||
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Qy       1917 TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA 1976
              ||  ||||||||||  |  |||||  |  |  |||  ||||||||||||||||  ||||||||||
Db       2620 TTGATCAGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA 2679

Qy       1977 GTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA 2036
             |||  ||||||||||||||||||||  |   ||  ||||||||||||||||||||  ||||  ||
Db       2680 GTATCCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACA 2739

Qy       2037 GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC------TAAAGAGGAAGTTCAT 2090
             |  ||||||||||||||||||||  ||||  ||||||||       |  |||||  ||  |    |
Db       2740 GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT 2799

Qy       2091 GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA 2150
              ||  |||||||  ||  ||  |||  ||  ||  ||  |   ||||||||||  |  ||  ||||||||
Db       2800 TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA 2859

Qy       2151 GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT 2210
             ||||||||||||||||   ||||||||||||||  |||||||  ||||||||||||||||
Db       2860 GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT 2919

Qy       2211 GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT 2270
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Qy       2271 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC 2330
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Db       2980 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC 3039

Qy       2331 ATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTA 2390
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Db       3040 ATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTA 3099

Qy       2391 TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC 2450
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Db       3100 TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC 3159

Qy       2451 TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC 2510
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Qy       2511 AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT 2570
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                ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||| |||
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Qy       2571 TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT 2630
                ||||||||||||||||| |||||||| ||||| |||||||| ||||||||||||||||||
Db       3280 TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT 3339

Qy       2631 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 2690
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3340 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 3399

Qy       2691 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT 2750
                ||||| ||||||||||||||| |||||||||| ||||||||||||||||||||||||
Db       3400 TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT 3459

Qy       2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
                |||||||||||||||||||||| |||||||||||| ||||||||||||||||||||
Db       3460 ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT 3519

Qy       2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
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Db       3520 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3579
```

RESULT 9
AAF90324
ID   AAF90324 standard; cDNA; 3579 BP.
XX
AC   AAF90324;
XX
DT   23-JUL-2001 (first entry)
XX
DE   Human NOGO-A cDNA.
XX
KW   NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;
KW   stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
KW   neuromuscular disorder; psychiatric disorder; developmental disorder;
KW   neuroprotective; nootropic; neuroleptic; antiparkinsonian;
KW   cerebroprotective; neuroleptic; diagnosis; therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200136631-A1.
XX
PD   25-MAY-2001.
XX
PF   14-NOV-2000; 2000WO-GB004345.
XX
PR   15-NOV-1999;   99GB-00026995.
PR   24-JAN-2000; 2000GB-00001550.
XX
PA   (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI   Michalovich D, Prinjha R;
XX
DR   WPI; 2001-343822/36.
DR   P-PSDB; AAB82349.

XX
PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
PT gene and may be useful in the treatment of neural disorders including
PT Alzheimer's and Parkinson's diseases.
XX
PS Disclosure; Page 25-26; 25pp; English.
XX
CC The present sequence is that of cDNA encoding human NOGO-A (see
CC AAB82349). NOGO-A is a previously known splice variant of the human NOGO
CC gene on chromosome 2p21. NOGO-A cDNA was obtained by PCR amplification of
CC human spinal cord cDNA. The invention relates to a novel splice variant,
CC NOGO-C (see AAF90323). It provides NOGO-C polypeptides and
CC polynucleotides, and methods for producing such polypeptides by
CC recombinant techniques. Also disclosed are methods for utilising NOGO-C
CC polypeptides and polynucleotides in the treatment of diseases including
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular
CC disorders, psychiatric disorders and developmental disorders. Also
CC provided are methods for identifying agonists and agonists for use in
CC treating conditions associated with NOGO-C imbalance, and diagnostic
CC assays for detecting diseases associated with inappropriate NOGO-C
CC activity or levels
XX
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Query Match 58.0%; Score 2223.6; DB 4; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy          1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
              || ||||||||||||||||||| |||| ||||||| |||||||||||| |||| || ||
Db        712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
              ||| | |||||||||||||||||| || || |   | ||||||||||||||   |||||
Db        772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
              |||||||||||| || | |  |||| ||| |||||||||| |||||||||| |||||
Db        832 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 891

Qy        181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
              |||||||||| |||||| ||||||| ||||| ||| |||||| |||||||| ||||||
Db        892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 951

Qy        241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
              |||||||||| |||||| | |||| | || |||| |||||||| | |||||||||  |
Db        952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy        301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
              |||||||||||| ||| || |||||| |||||| ||||| |||| ||| |||| ||
Db       1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy        361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
              ||   |||| ||||| |||||||| |||| |||||||||| |||||| |||||||||
Db       1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1128
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Qy        421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
              |||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

Qy        481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
              ||||||| |   ||| |||||||||| | |||  |||||||||||| || ||||||||
Db       1189 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC 1245

Qy        541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
              |||||| |||||||||||||| |||   ||| |||||||||||| ||||| ||||  |||
Db       1246 TTGGAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAA 1305

Qy        601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
              |||||||||| || |||||||||| ||||| || |||||||| ||||||| | |||
Db       1306 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG 1365

Qy        661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGTT 717
              | | || | ||||| || ||||| ||||||||||||||||   || |||||||||   ||
Db       1366 GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1425

Qy        718 TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
               |||||||||||||||| ||||| | ||||| |||||| |||||||||| |||||||||
Db       1426 GCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA 1485

Qy        778 AAGATAGAA-AAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA 836
              || |||||| |||| ||||| ||||| |||||||||||||| | ||   ||| ||||||
Db       1486 AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA 1545

Qy        837 AACCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG 896
              |||||||| ||| | |||||||||| ||| |||||||||| || ||||||||| || |
Db       1546 AACCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA 1605

Qy        897 TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGTT 956
               |||||||||| |||||||| |||||||||||||||||||| || || |||||||| ||
Db       1606 ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA 1665

Qy        957 CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA 1016
              |||||||||||||||||||||||||||||| |||||||||||| ||||| | |||||||
Db       1666 CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA 1725

Qy       1017 AAAATGGACCTGGTTCAAACTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG 1076
              ||||||||| |||||||||| ||||||| | |||| |||||||| || |||| | |||||
Db       1726 AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG 1785

Qy       1077 CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC 1136
              |||||||||| |||||||| || |||||||||| ||||| ||||||||||||||||||
Db       1786 CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT 1845

Qy       1137 ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT 1196
              |||||||||||||| ||||||| |||||||||||||||||||| |   | |||| |||
Db       1846 ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC 1905

Qy       1197 TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA 1256
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Db       1906 TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA 1962

Qy       1257 AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAAGAATCAGGAATGAAT 1316
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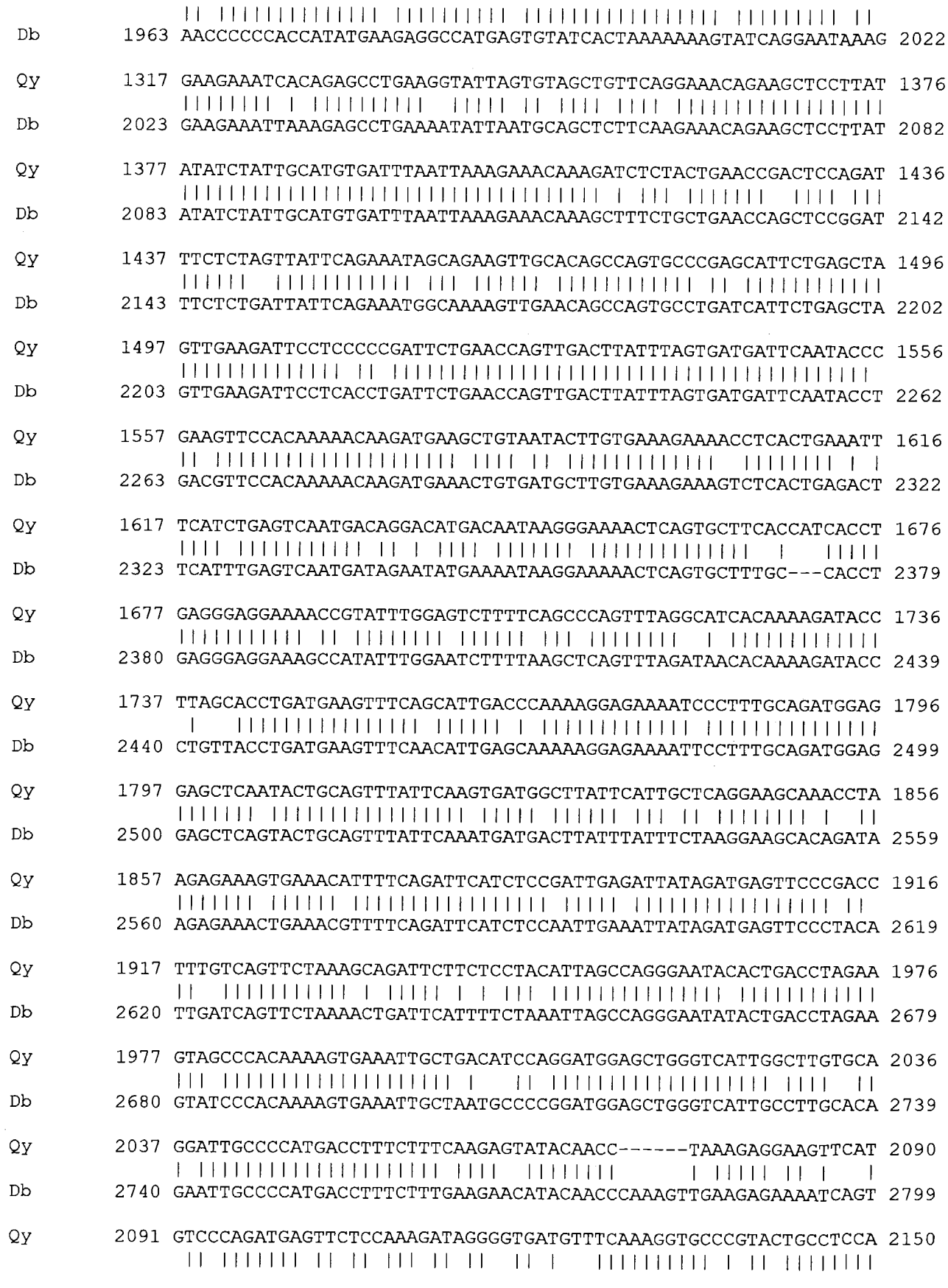

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Db       2800 TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA 2859

Qy       2151 GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT 2210
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Db       2860 GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT 2919

Qy       2211 GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT 2270
             |||||||||||  ||||  ||||||||||||  ||||||||||||||    |||||  ||||||
Db       2920 GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT 2979

Qy       2271 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC 2330
             |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       2980 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC 3039

Qy       2331 ATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTA 2390
             |||||||||||||||||||||||||||||||| | ||||||||||| ||  ||||||||
Db       3040 ATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTA 3099

Qy       2391 TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC 2450
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Db       3100 TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC 3159

Qy       2451 TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC 2510
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Db       3160 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC 3219

Qy       2511 AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT 2570
             |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       3220 AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT 3279

Qy       2571 TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT 2630
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Db       3280 TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT 3339

Qy       2631 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 2690
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3340 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 3399

Qy       2691 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT 2750
             |||||  ||||||||||||||||  ||||||||||  ||||||||||||||||||||||||
Db       3400 TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT 3459

Qy       2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
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Db       3460 ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT 3519

Qy       2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
             |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       3520 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3579
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RESULT 10
ABK90134
ID   ABK90134 standard; DNA; 3579 BP.
XX
AC   ABK90134;
XX
```

DT 21-OCT-2002 (first entry)
XX
DE DNA encoding human NogoA protein.
XX
KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;
KW Nogo-associated disease; metastasis; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .3579
FT /*tag= a
FT /product= "Human NogoA protein"
XX
PN WO200257483-A2.
XX
PD 25-JUL-2002.
XX
PF 18-JAN-2002; 2002WO-GB000228.
XX
PR 18-JAN-2001; 2001GB-00001312.
XX
PA (GLAX) GLAXO GROUP LTD.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Blackstock WP, Hale RS, Prinjha R, Rowley A;
XX
DR WPI; 2002-599722/64.
DR P-PSDB; ABG30938.
XX
PT Identifying modulators of Nogo or BACE activity for treating acute
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
PT providing and monitoring interaction between Nogo and BACE polypeptides.
XX
PS Disclosure; Page 53-58; 68pp; English.
XX
CC The present invention relates to a new method of identifying modulators
CC of Nogo function or BACE activity. The method involves providing Nogo and
CC BACE polypeptides capable of binding with each other, monitoring the
CC interaction between these polypeptides, and determining if the test agent
CC is a modulator of Nogo or BACE activity. The method is useful in treating
CC acute neuronal injuries, such as spinal or head injury, stroke,
CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,
CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.
CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue
CC hypertrophy) of the central nervous system. The BACE polypeptide is
CC useful in screening methods to identify agents that may act as modulators
CC of BACE activity and in particular agents that may be useful in treating
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
CC and the polynucleotide encoding the BACE polypeptide are useful in
CC manufacturing a medicament for the treatment or prevention of disorders
CC responsive to the modulation of Nogo activity, in alleviating the
CC symptoms or improving the condition of a patient suffering from this

CC disorder, in axon regeneration, or in preventing metastasis or spreading
CC of a cancer. The polynucleotide may also be an essential component in
CC assays, a probe, in recombinant protein synthesis, and in gene therapy
CC techniques. The present nucleic acid sequence encodes the human NogoA
CC protein of the invention
XX
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Query Match 58.0%; Score 2223.6; DB 6; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy          1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
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Db        712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
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Db        772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
              |||||||||||||| || | |  |||| ||| |||||||||| |||||||||| |||||
Db        832 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 891

Qy        181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
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Db        892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 951

Qy        241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
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Db        952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy        301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
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              ||   |||| ||||| |||||||| |||| |||||||||| |||||| |||||||||
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Qy        421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
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Db       1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

Qy        481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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Db       1189 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC 1245

Qy        541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
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Db       1246 TTGGAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAA 1305

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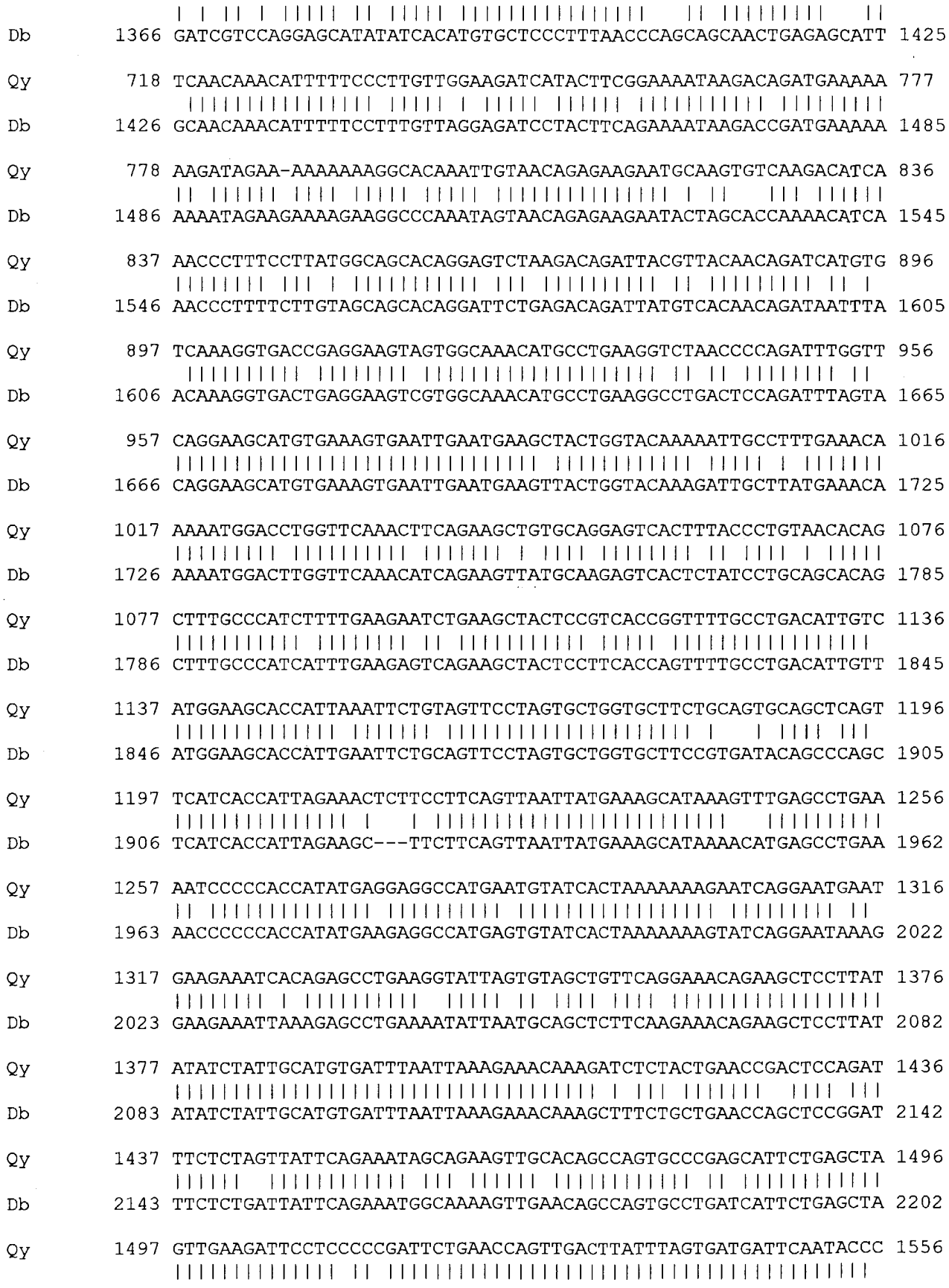

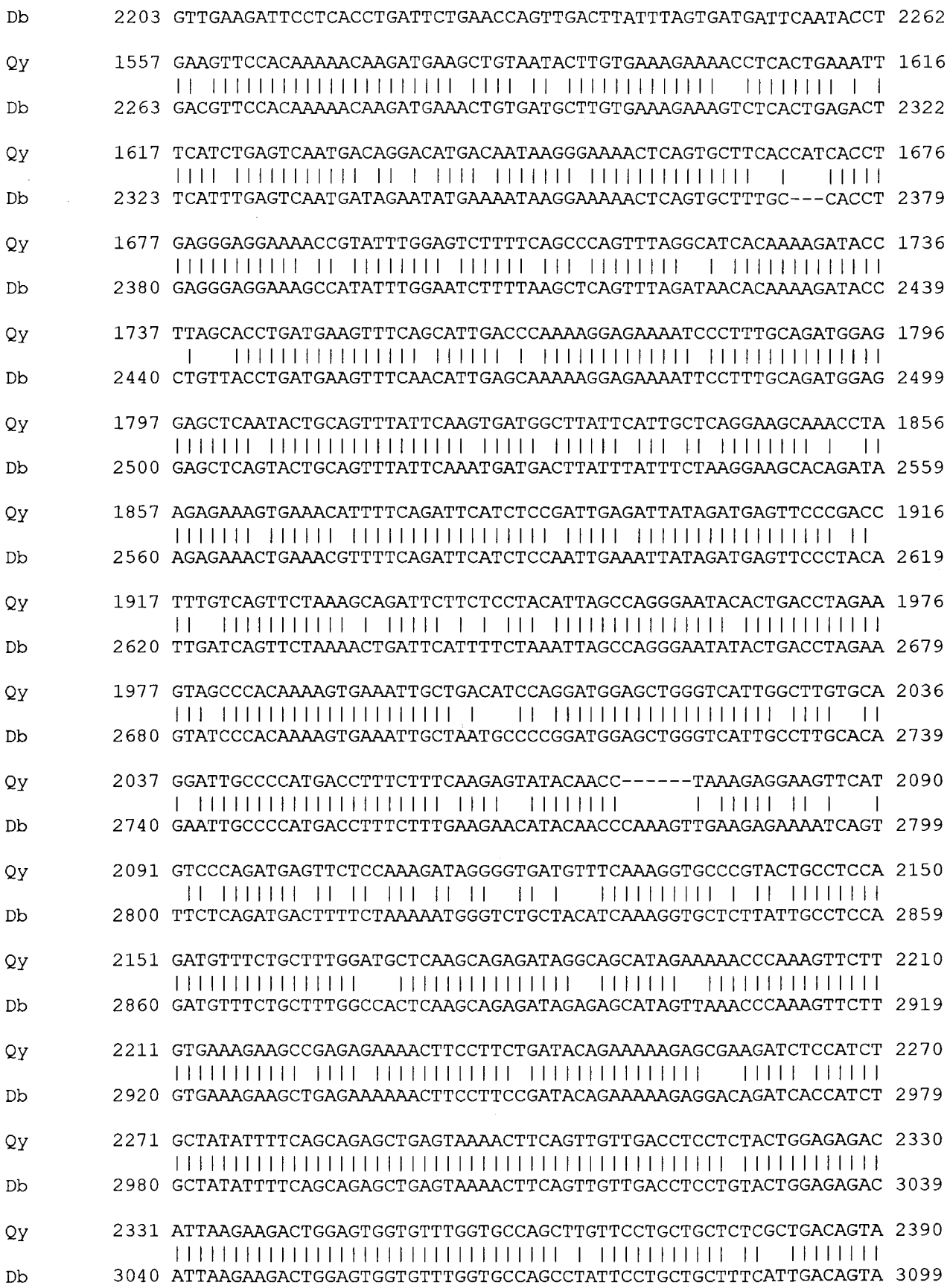

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Qy       2451 TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC 2510
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Db       3160 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC 3219

Qy       2511 AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT 2570
             ||||||||| |||||||||||||||||||||||||||||||||||||||||||||| |||
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             |||||||||||||||| |||||||| ||||| |||||||| ||||||||||||||||||
Db       3280 TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT 3339

Qy       2631 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 2690
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Db       3340 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 3399

Qy       2691 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT 2750
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Db       3400 TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT 3459

Qy       2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
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Qy       2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
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RESULT 11
ABN86601
ID   ABN86601 standard; DNA; 3579 BP.
XX
AC   ABN86601;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Human neurotransmitter receptor protein Nogo encoding DNA.
XX
KW   Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW   central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW   vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW   nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW   osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW   neurotransmitter receptor; human; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3579
FT                   /*tag=  a
FT                   /product= "Nogo"
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FT /note= "Nogo-A, Nogo-B and Nogo-C"
XX
PN US2002072493-A1.
XX
PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-00893348.
XX
PR 19-MAY-1998; 98IL-00124500.
PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.
PR 19-MAY-1999; 99US-00314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR P-PSDB; ABB81078, ABB81079, ABB81080.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.
XX
PS Disclosure; Page 49-53; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents a DNA
CC encoding the human neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B
CC and Nogo-C), an example of NS-specific antigen

XX
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Query Match 58.0%; Score 2223.6; DB 6; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy          1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
              || |||||||||||||||||| |||| ||||||| |||||||||||| |||| || ||
Db        712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
              ||| | |||||||||||||||||| || || |   | |||||||||||||   |||||
Db        772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
              |||||||||||||  || | |  |||| ||| |||||||||| |||||||||| |||||
Db        832 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 891

Qy        181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
              |||||||||| |||||| ||||||| ||||| ||| |||||| |||||||| ||||||
Db        892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 951

Qy        241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
              |||||||||| |||||| | |||| | || |||| |||||||| | |||||||||  |
Db        952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy        301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
              |||||||||||||| ||| || |||||| |||||| ||||| |||| ||| |||| ||
Db       1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy        361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
              ||   |||| ||||| |||||||| |||| |||||||||| |||||| |||||||||
Db       1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1128

Qy        421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
              |||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

Qy        481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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Db       1306 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG 1365

Qy        661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGTT 717
              | | || | ||||| || ||||| ||||||||||||||||   || |||||||||   ||
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Qy        718 TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
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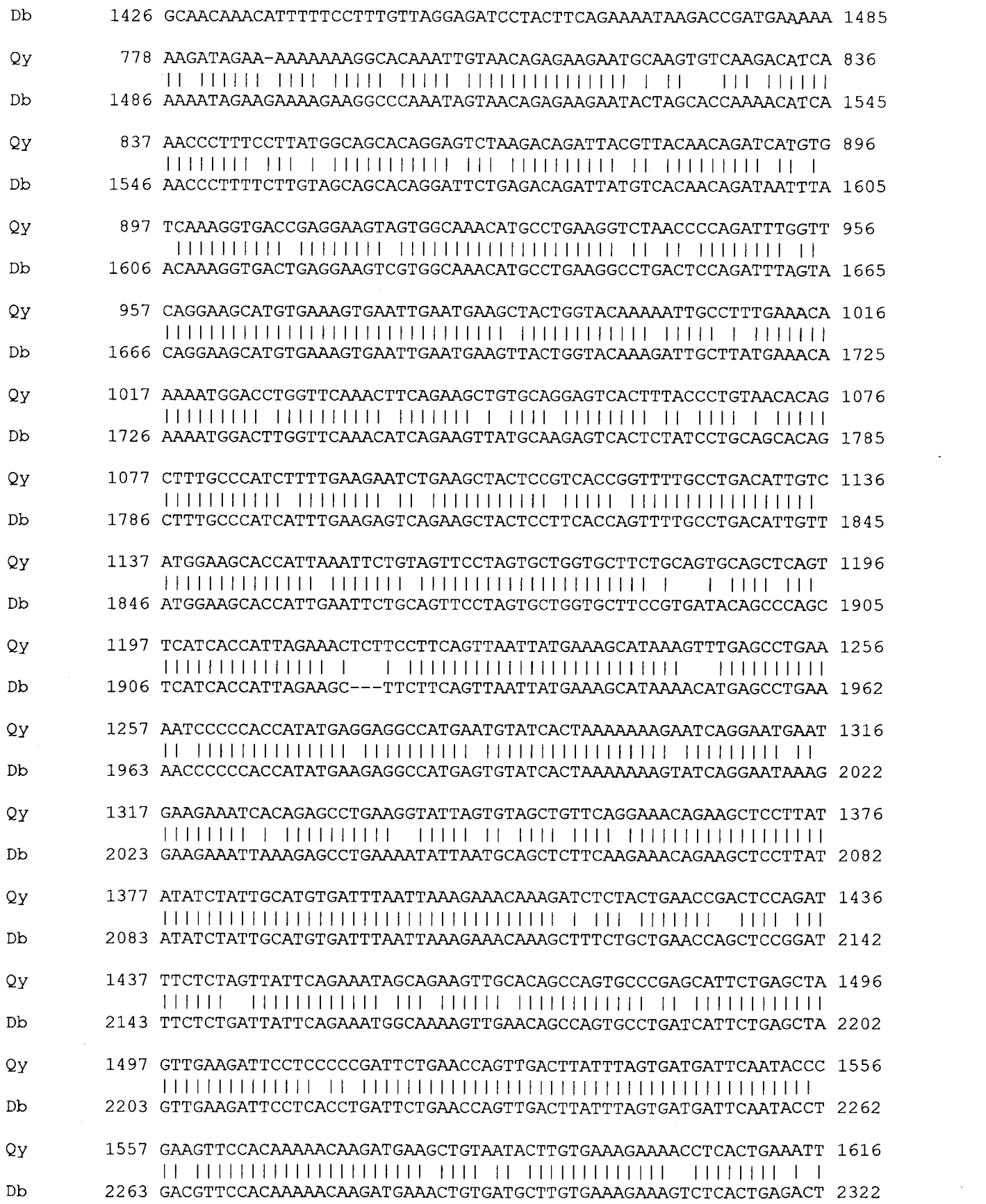

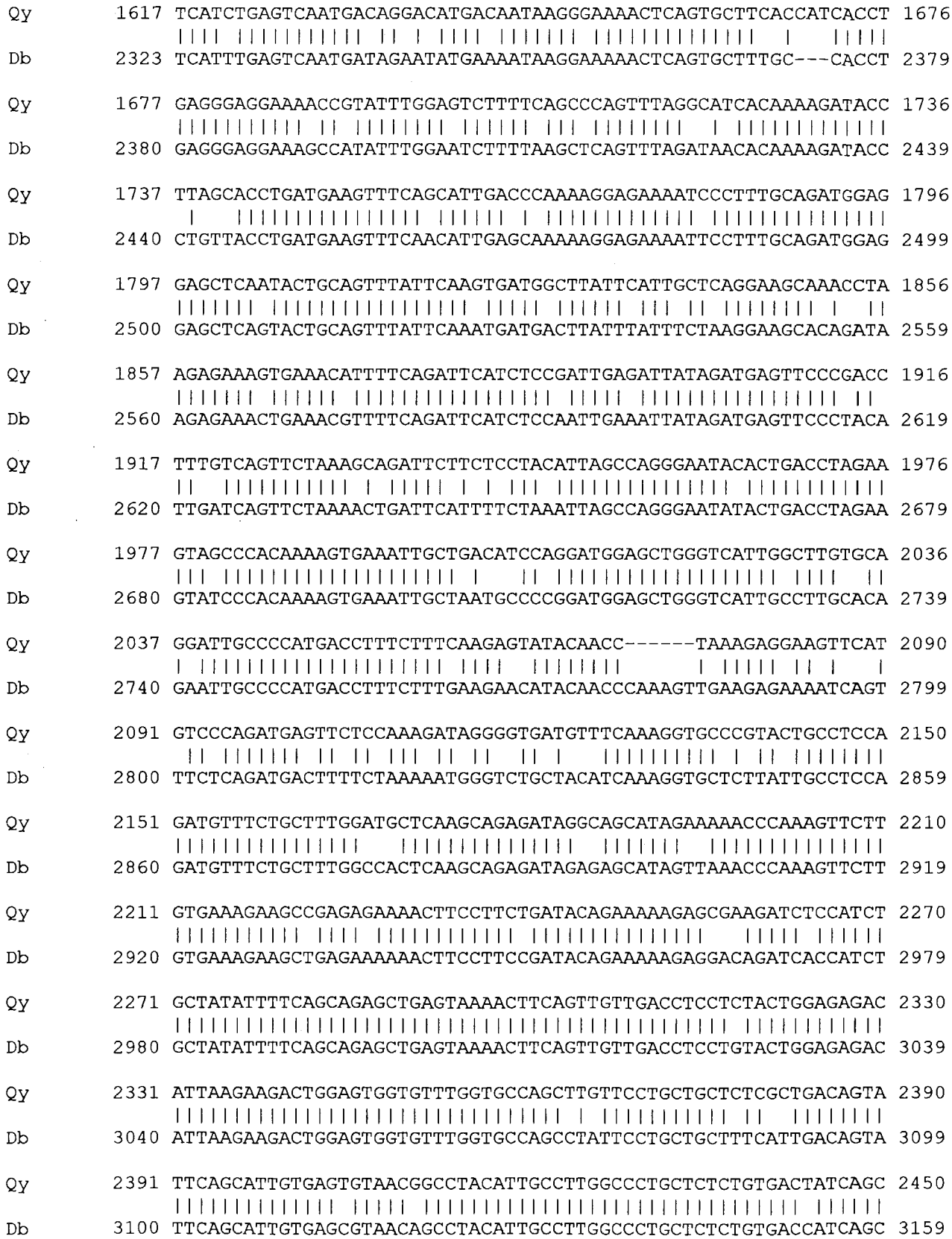

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Qy       2511 AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT 2570
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Qy       2571 TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT 2630
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Db       3280 TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT 3339

Qy       2631 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 2690
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Db       3340 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 3399

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Qy       2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
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Qy       2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
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RESULT 12
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ID   AAD01173 standard; cDNA; 4684 BP.
XX
AC   AAD01173;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat neurite growth inhibitor Nogo A cDNA.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
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PN   WO200031235-A2.
XX
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PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
DR P-PSDB; AAY71310.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 26; Fig 2A; 122pp; English.
XX
CC The present sequence is a cDNA encoding rat Nogo A protein which is a
CC potent neural cell growth inhibitor and is free of all central nervous
CC system (CNS) myelin material with which it is natively associated. The
CC present sequence was generated by fusing RO18U37-3, R1-3U21 cDNA
CC sequences isolated from hexanucleotides-primed rat brain stem/spinal cord
CC library, and Oli18 cDNA from an oligo d(T)-primed rat oligodendrocyte
CC library. Nogo proteins and fragments displaying neurite growth inhibitory
CC activity are used in the treatment of neoplastic disease of the CNS e.g.
CC glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve
CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
CC promote Nogo activity can be used to treat or prevent hyperproliferative
CC or benign dysproliferative disorders e.g. psoriasis and tissue
CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
CC inhibit production of Nogo protein to induce regeneration of neurons or
CC to promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However the specification does not include sequences for
CC these SEQ ID numbers
XX
SQ Sequence 4684 BP; 1358 A; 1048 C; 1112 G; 1166 T; 0 U; 0 Other;

Query Match 57.0%; Score 2183.4; DB 3; Length 4684;
Best Local Similarity 78.0%; Pred. No. 0;
Matches 3004; Conservative 0; Mismatches 736; Indels 109; Gaps 27;

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Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
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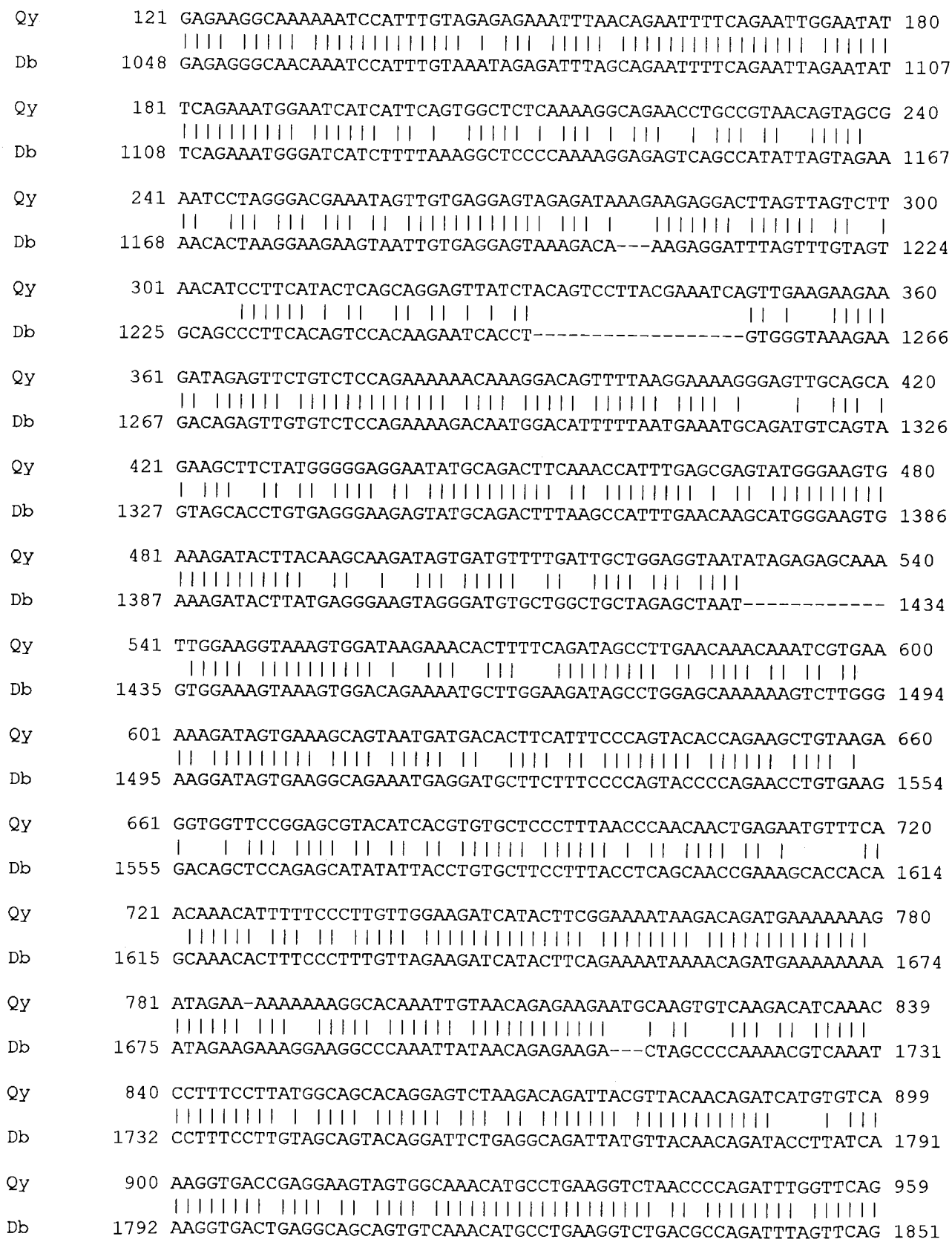

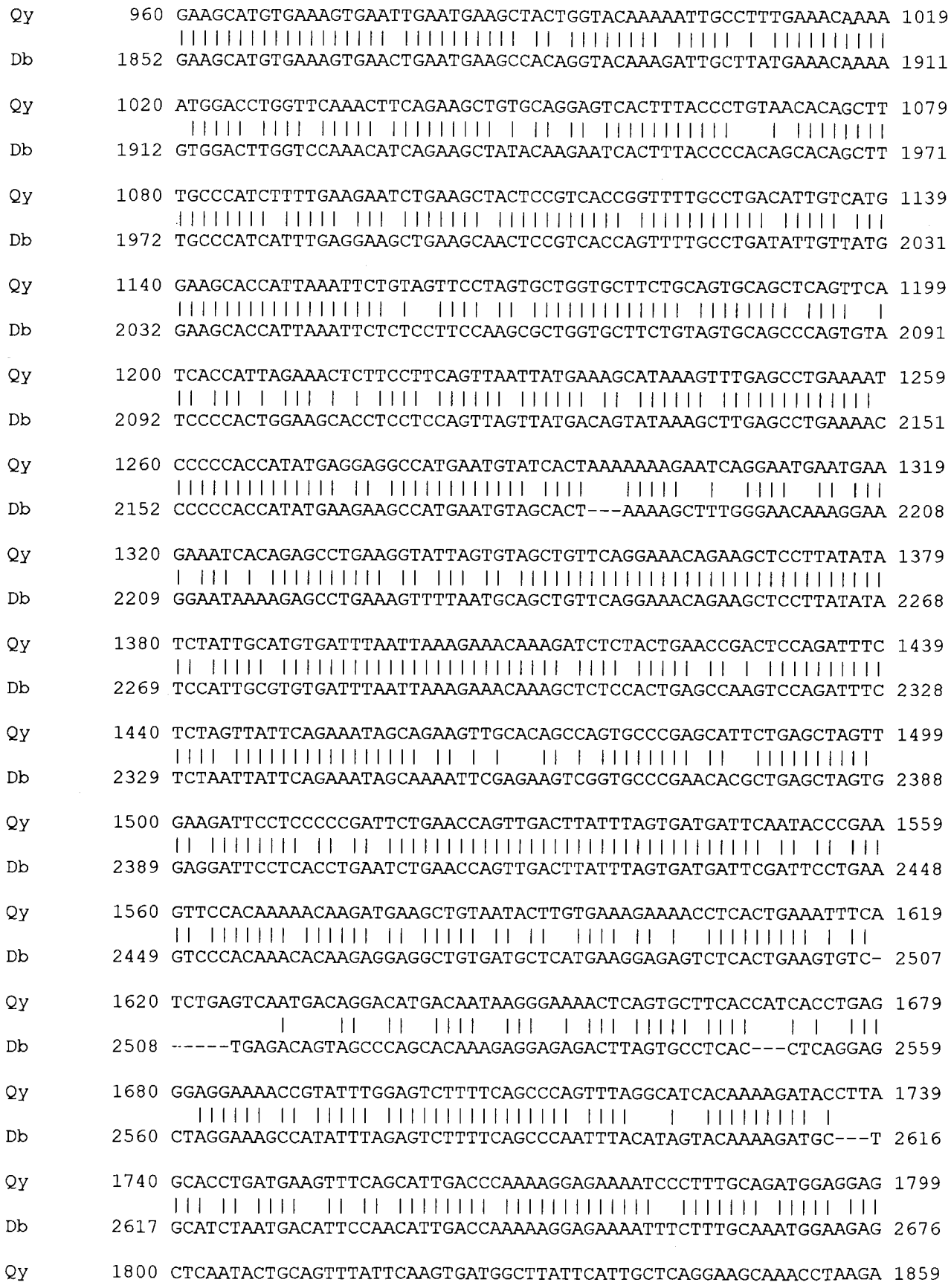

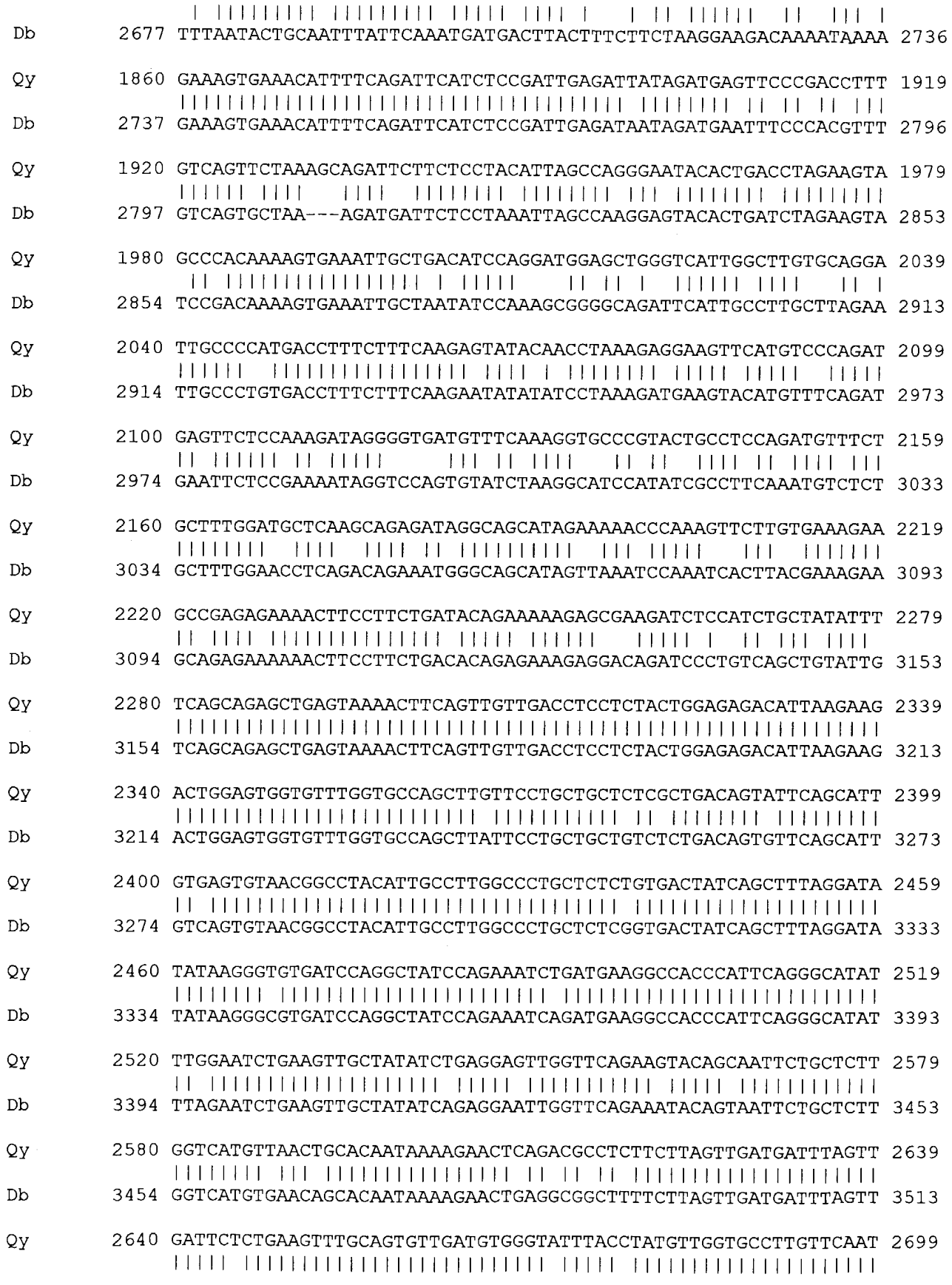

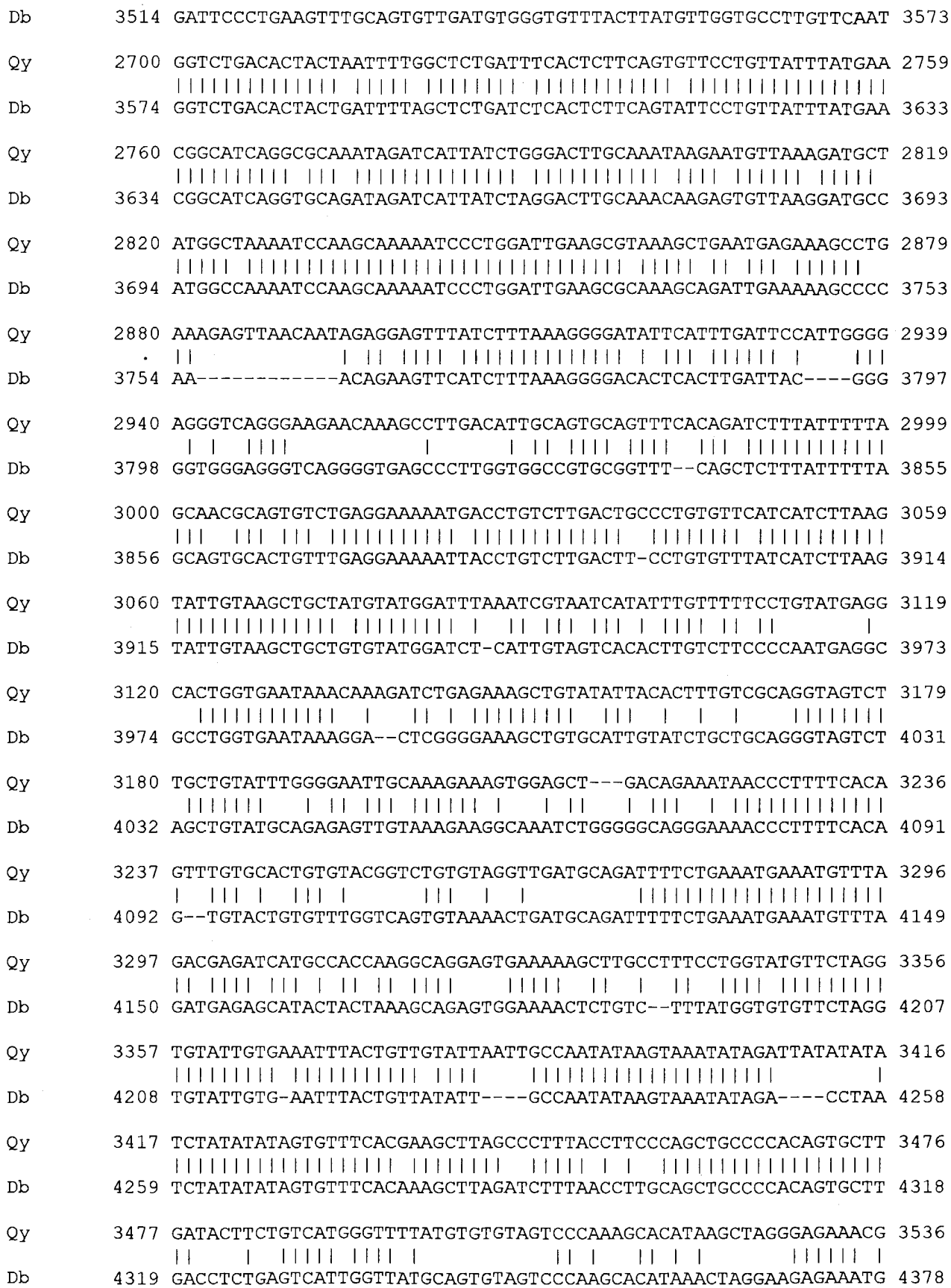

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Db       4379 TATTTGTAGGAGTGCTACCTACCACCTGTTTTCAAGAAAATATAGAACTCCAACAAAAAT 4438

Qy       3596 CCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTC----- 3650
                 ||  | |  |  |   |  |   | ||||||||||| ||||| ||||
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Qy       3651 -----TGGACTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTA 3705
                  |||||||||| | |||||||| |||||||||| |||||||||||||||| |
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Qy       3706 AGAAAATAT-AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGT 3764
              |||||  || |||||| || |||||| |||||||||||||| ||| |||| |  ||||||
Db       4557 AGAAATCATAAAATGAAGACTTATACCATTGTGGTTTAAGCCGTACTGAATT--ATCTGT 4614

Qy       3765 GGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAA 3824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4615 GGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAA 4674

Qy       3825 AAAAAAAAA 3833
              |||||||||
Db       4675 AAAAAAAAA 4683
```

```
RESULT 13
ABN86600
ID   ABN86600 standard; DNA; 4684 BP.
XX
AC   ABN86600;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Rat neurotransmitter receptor protein Nogo encoding DNA.
XX
KW   Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW   central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW   vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW   nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW   osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW   neurotransmitter receptor; rat; gene; ds.
XX
OS   Rattus norvegicus.
XX
FH   Key             Location/Qualifiers
FT   CDS             253. .3744
FT                   /*tag=  a
FT                   /product= "Nogo-A"
XX
PN   US2002072493-A1.
XX
PD   13-JUN-2002.
XX
PF   28-JUN-2001; 2001US-00893348.
XX
PR   19-MAY-1998;   98IL-00124500.
```

PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.
PR 19-MAY-1999; 99US-00314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR P-PSDB; ABB81074, ABB81076, ABB81077.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.
XX
PS Disclosure; Page 40-44; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents a DNA
CC encoding the rat neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B
CC and Nogo-C), an example of NS-specific antigen
XX
SQ Sequence 4684 BP; 1358 A; 1047 C; 1112 G; 1167 T; 0 U; 0 Other;

Query Match 56.9%; Score 2179.4; DB 6; Length 4684;
Best Local Similarity 78.2%; Pred. No. 0;
Matches 3008; Conservative 0; Mismatches 731; Indels 110; Gaps 28;

Qy 1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
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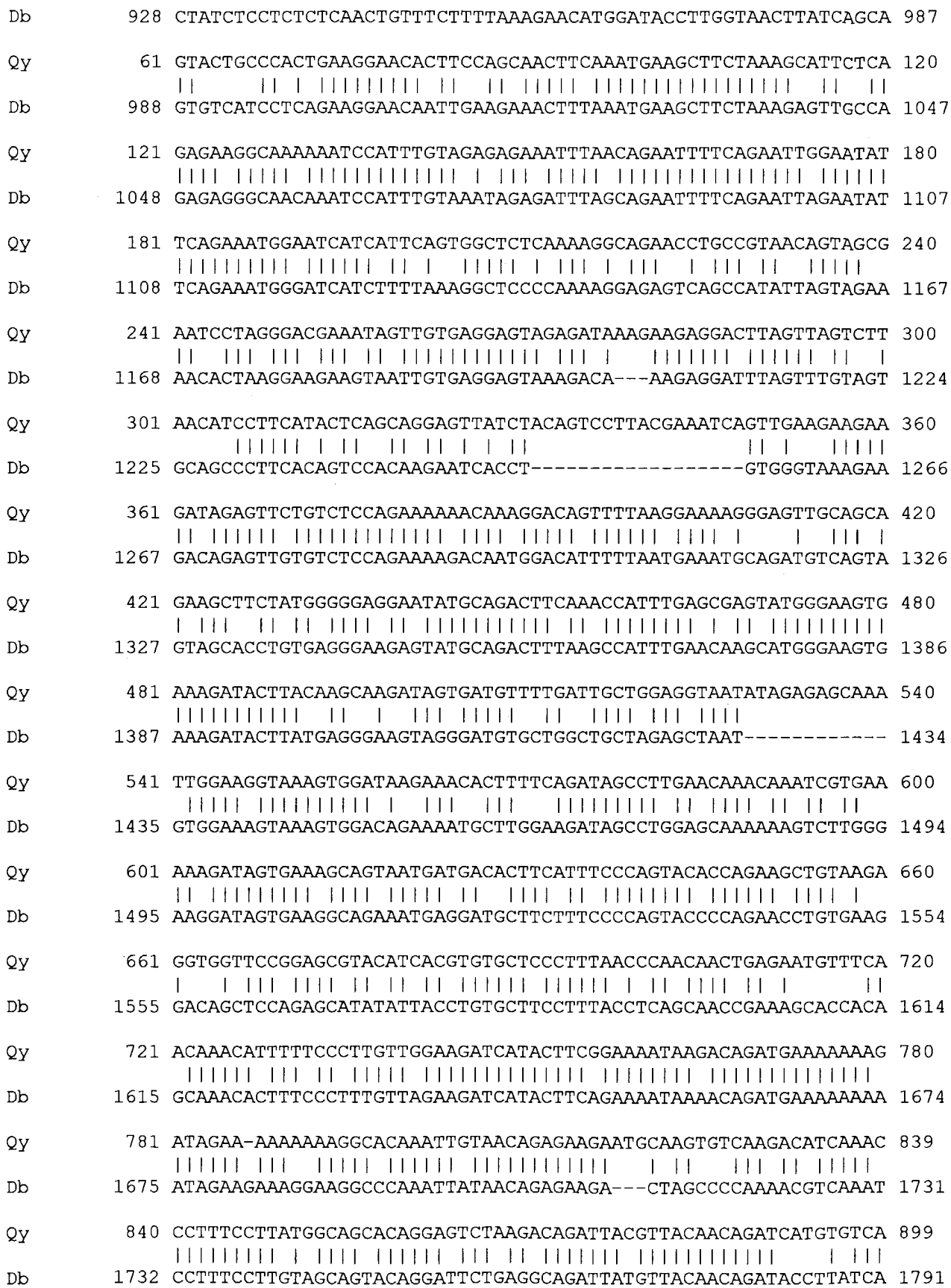

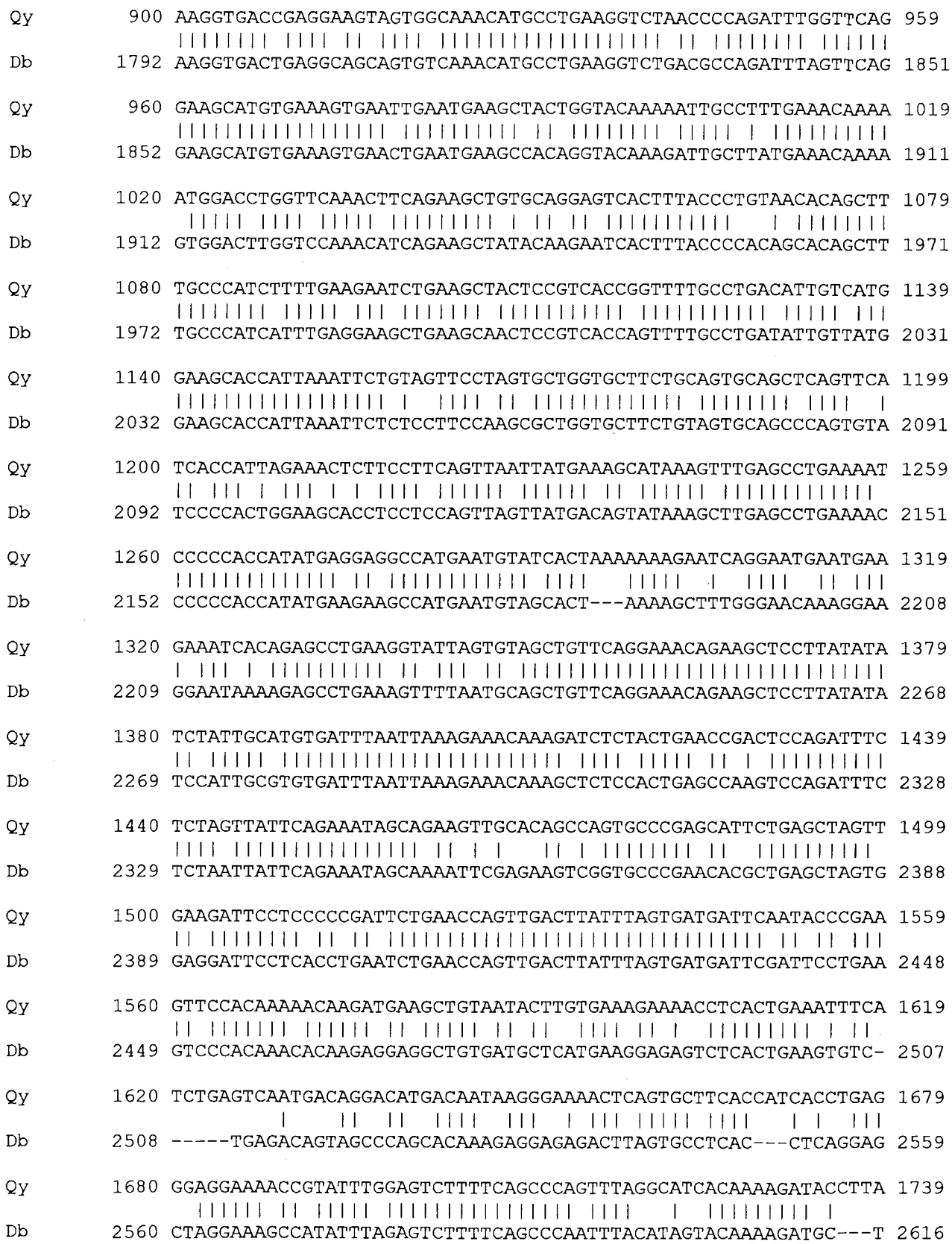

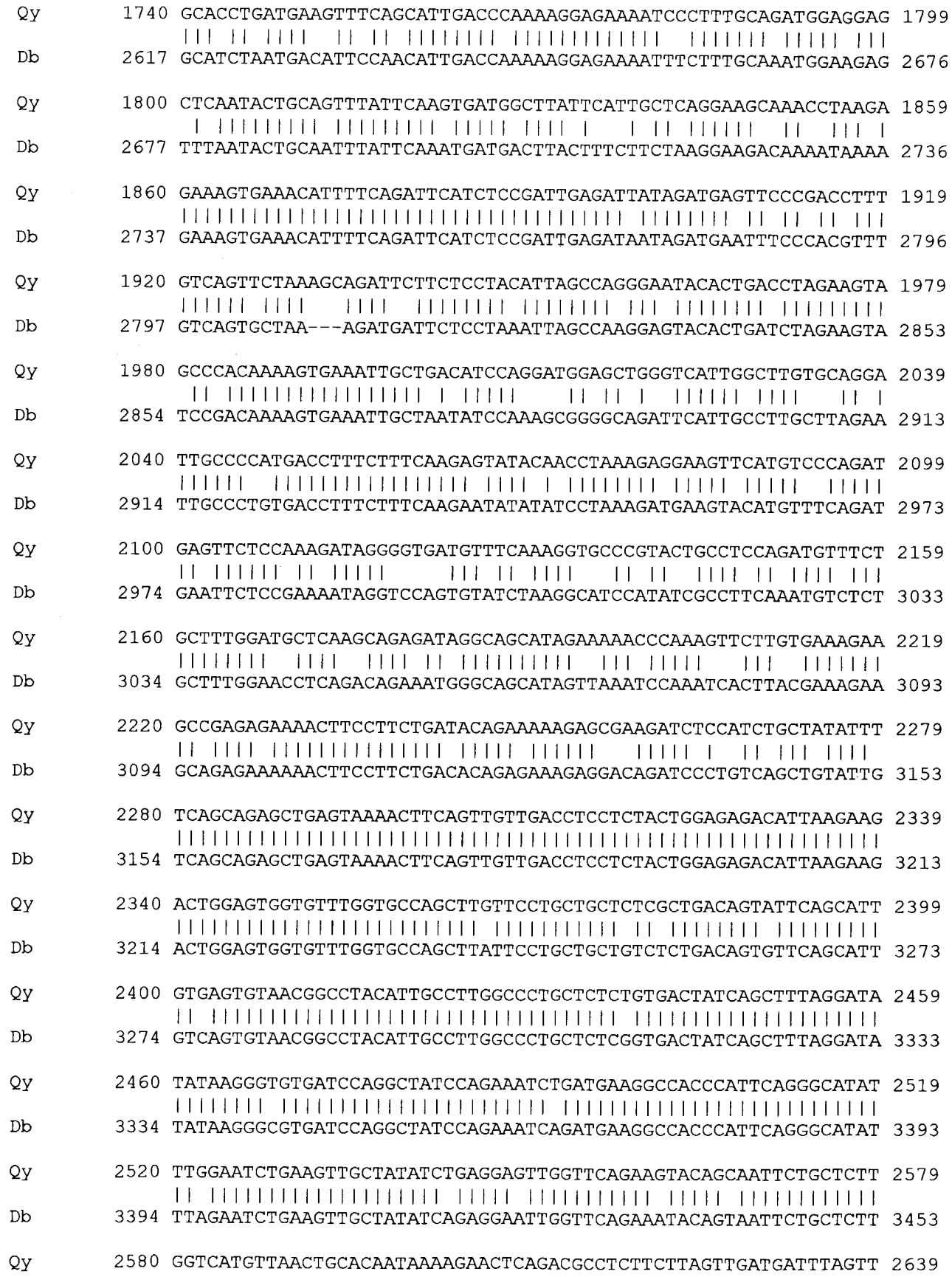

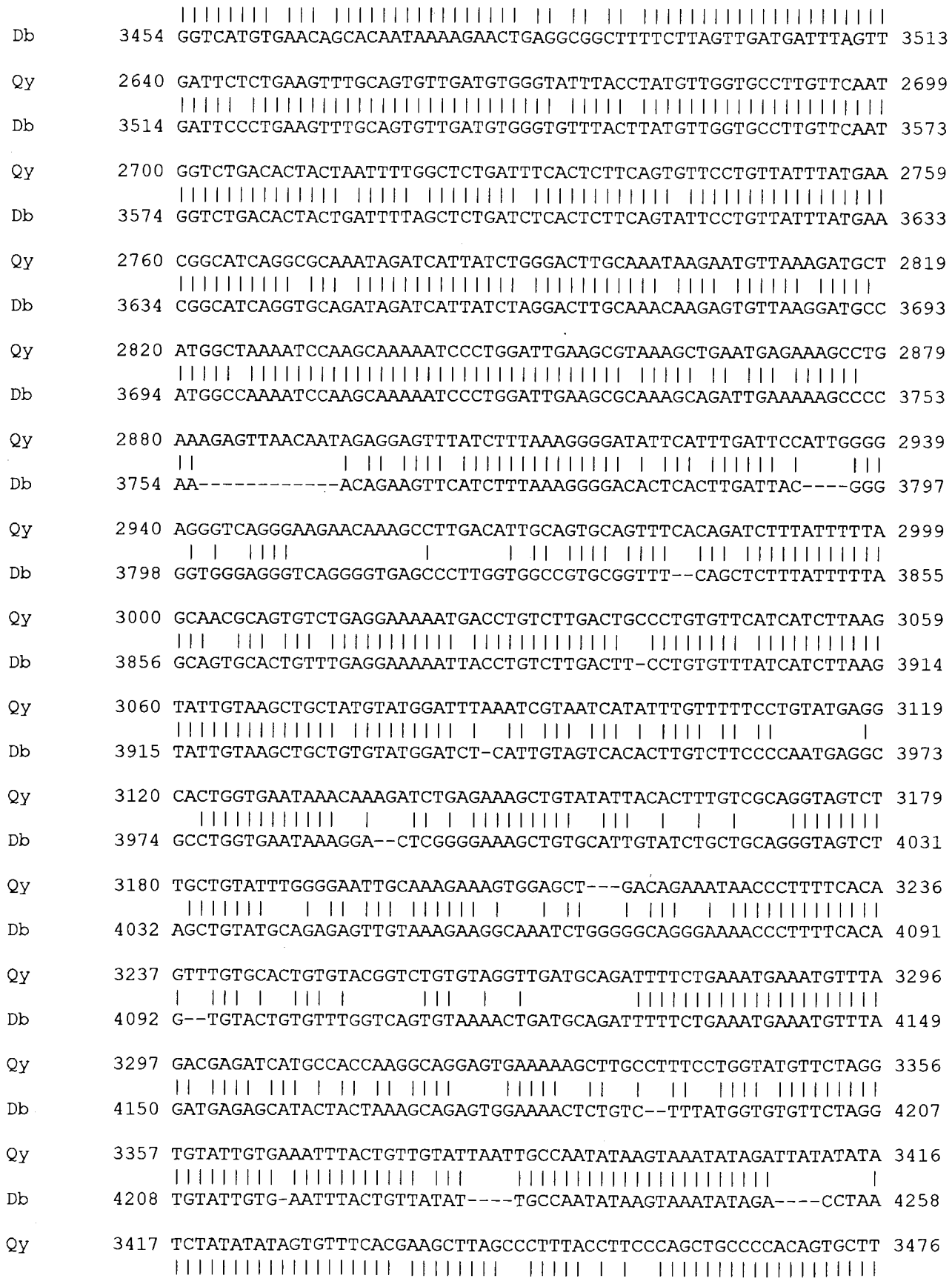

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Db       4259 TCTATATATAGTGTTTCACAAAGCTTAGATCTTTAACCTTGCAGCTGCCCCACAGTGCTT 4318

Qy       3477 GATACTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACG 3536
              ||    |  ||||| |||| |    ||||||||| |   || | |       |||||| |
Db       4319 GACCTCTGAGTCATTGGTTAT-GCAGTGTAGTCCAAGCACATAAACTAGGAAGAGAAATG 4377

Qy       3537 TACTTCTAGGCGCACTACC-ATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACT 3595
              || || |||| |  ||||| | |   | |   || |||   |    |  | |||| || |
Db       4378 TATTTGTAGGAGTGCTACCTACCACCTGTTTTCAAGAAAATATAGAACTCCAACAAAAAT 4437

Qy       3596 CCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTC----- 3650
                  ||  | |  |  |   |  |   |   | |||||||||| ||||| ||||
Db       4438 ATAGAATGTCATTTCAAAGACTTACTGTATGTATAGTTAATTTTGTCACAGACTCTGAAA 4497

Qy       3651 -----TGGACTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTA 3705
                  |||||||||| | ||||||||  |||||||||| |||||||||||||||| |
Db       4498 TTCTATGGACTGAATTTCATGCTTCC--AAATGTTTGCAGTTATCAAACATTGTTATGCA 4555

Qy       3706 AGAAAATAT-AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGT 3764
              |||||  || |||||| || |||||| |||||||||||||| ||| |||| |  ||||||
Db       4556 AGAAATCATAAAATGAAGACTTATACCATTGTGGTTTAAGCCGTACTGAATT--ATCTGT 4613

Qy       3765 GGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAA 3824
              |||||||||||||||||||||||||||||||||||||||||||||||||  | ||||||||
Db       4614 GGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGATCTTAAAAAAAA 4673

Qy       3825 AAAAAAAAA 3833
              |||||||||
Db       4674 AAAAAAAAA 4682
```

```
RESULT 14
AAV30920
ID   AAV30920 standard; cDNA; 2386 BP.
XX
AC   AAV30920;
XX
DT   14-SEP-1998  (first entry)
XX
DE   Human secreted protein BG160_1 cDNA.
XX
KW   BG160_1; secreted protein; protein factor; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             102. .2030
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FT   sig_peptide     1863. .1899
FT                   /*tag=  b
FT                   /note= "putative leader/signal peptide"
FT   mat_peptide     1900. .2027
FT                   /*tag=  c
XX
PN   WO9817687-A2.
XX
PD   30-APR-1998.
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XX
PF 24-OCT-1997; 97WO-US019590.
XX
PR 25-OCT-1996; 96US-00740274.
PR 24-OCT-1997; 97US-00740274.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agostino MJ;
XX
DR WPI; 1998-261426/23.
DR P-PSDB; AAW58383.
XX
PT Nucleic acid encoding secreted protein from human cells - useful, e.g. as
PT immuno-modulators, anti-tumour agents, promoters of tissue growth,
PT haemostatic and thrombolytic agents etc.
XX
PS Claim 20; Page 74-75; 114pp; English.
XX
CC This cDNA clone, designated BG160_1, codes for a novel human secreted
CC protein (see AAW58383). It was isolated from a human adult brain cDNA
CC library using methods selective for cDNAs that encode secreted proteins.
CC The clone is deposited in composite clone ATCC 98232; an oligonucleotide
CC (see AAT99725) is designed to isolate the clone from the composite. The
CC predicted AT415_4 amino acid sequence shows homology to neuroendocrine-
CC specific proteins. Novel cDNA clones (see AAV30916-32) coding for human
CC secreted proteins (see AAW58580-90) are claimed. These can be used for
CC recombinant production of the secreted proteins for analysis,
CC characterisation, diagnostic or therapeutic use. They can also be used as
CC tissue or mol.wt. markers, for chromosome identification, to identify
CC genetic disorders, to isolate new related DNA, as sources of primers for
CC PCR, to generate antibodies, and in interaction trap assays. The secreted
CC proteins may also have many biological activities, e.g. cytokine,
CC immunomodulator, haematopoiesis regulating activity, tissue growth
CC activity, activin or inhibin activity, chemotactic or chemokinetic
CC activity, haemostatic and thrombolytic activity, receptor/ligand
CC activity, antiinflammatory, cadherin and tumour invasion suppressor
CC activity, and tumour inhibition activity. The proteins can be expressed
CC in vivo from DNA, introduced in gene therapy vectors
XX
SQ Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 U; 0 Other;

Query Match 46.4%; Score 1777.2; DB 2; Length 2386;
Best Local Similarity 86.9%; Pred. No. 0;
Matches 2101; Conservative 0; Mismatches 258; Indels 59; Gaps 11;

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Qy        827 CAAGACATCAAACCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAAC 886
              ||| |||||||||||||| ||| | |||||||||| ||| |||||||||| || |||||
Db          2 CAAAACATCAAACCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAAC 61

Qy        887 AGATCATGTGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCC 946
              |||| || |  |||||||||| |||||||| |||||||||||||||||| || || ||
Db         62 AGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCC 121

Qy        947 AGATTTGGTTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGC 1006
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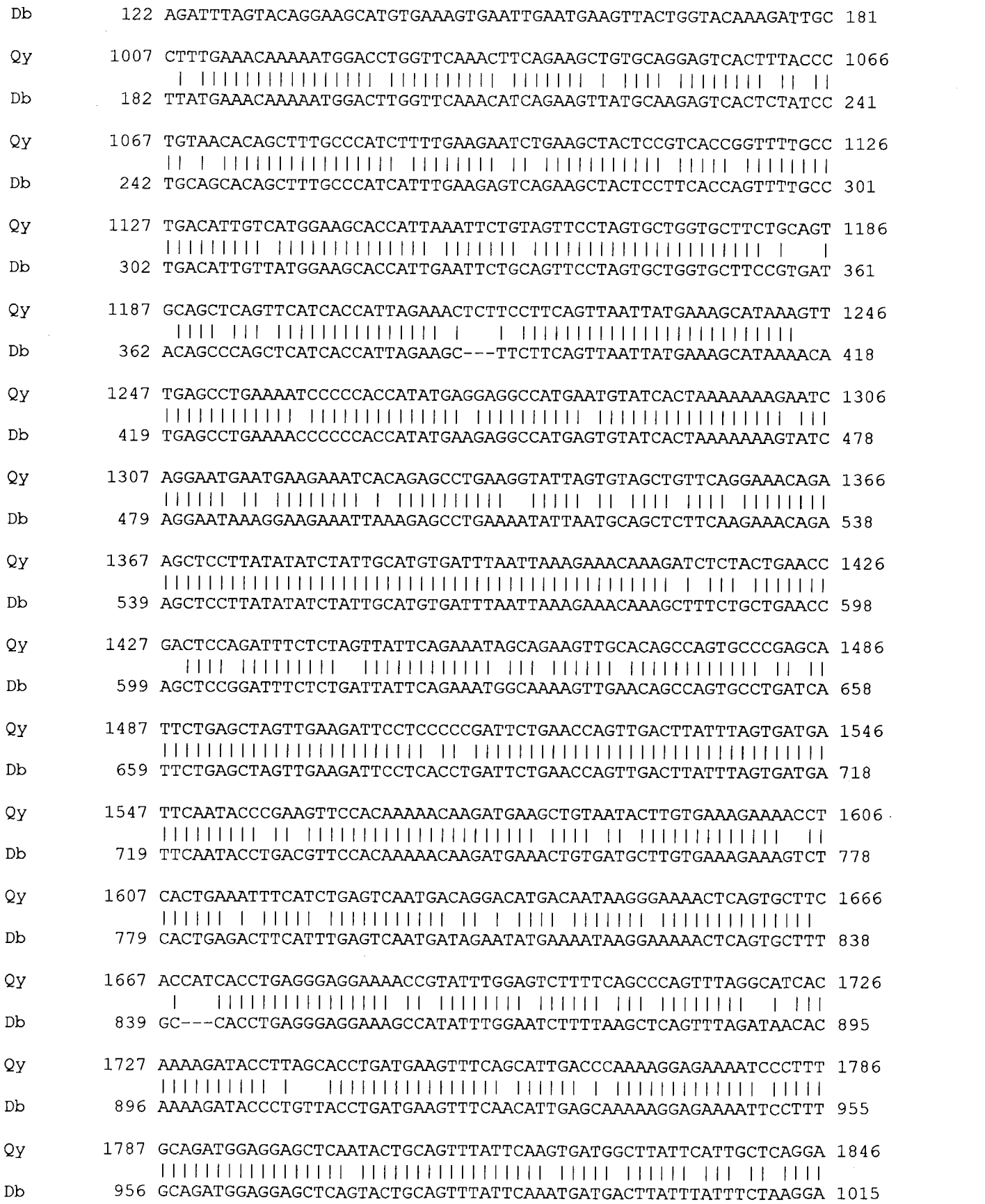

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Db       1016 AGCACAGATAAGAGAAACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGA 1075

Qy       1907 GTTCCCGACCTTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACAC 1966
Db       1076 GTTCCCTACATTGATCAGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATAC 1135

Qy       1967 TGACCTAGAAGTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATT 2026
Db       1136 TGACCTAGAAGTATCCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATT 1195

Qy       2027 GGCTTGTGCAGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGT 2086
Db       1196 GCCTTGCACAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGA 1255

Qy       2087 TCA------TGTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGT 2140
Db       1256 GAAAATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTT 1315

Qy       2141 ACTGCCTCCAGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACC 2200
Db       1316 ATTGCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACC 1375

Qy       2201 CAAAGTTCTTGTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAG 2260
Db       1376 CAAAGTTCTTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAG 1435

Qy       2261 ATCTCCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTA 2320
Db       1436 ATCACCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTA 1495

Qy       2321 CTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTGTTCCTGCTGCTCTC 2380
Db       1496 CTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTC 1555

Qy       2381 GCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGT 2440
Db       1556 ATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGT 1615

Qy       2441 GACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGG 2500
Db       1616 GACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGG 1675

Qy       2501 CCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAA 2560
Db       1676 CCACCCATTCAGG---------------GAAGTTGCTATATCTGAGGAGTTGGTTCAGAA 1720

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Db       1721 GTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTT 1780

Qy       2621 CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTA 2680
Db       1781 CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTA 1840
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Db       1901 TGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAA 1960

Qy       2801 TAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAA 2860
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Db       1961 TAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAA 2020

Qy       2861 AGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATAT 2920
             |||||||||| || |||  ||| | |||       ||||||| ||||||||||||||||
Db       2021 AGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATAT 2075

Qy       2921 TCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTT 2980
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Db       2076 TCATTTGATTATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTT 2134

Qy       2981 TCAC-----------AGATCTTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCT 3028
             ||||           |||||||||||||||| | ||| || | |||||||||| ||||
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Qy       3029 GTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAA 3088
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2195 GTCTTGACTGCCATGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAA 2254

Qy       3089 TCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAA 3148
              |||||||||  | |||||||| | ||||||||||||| |           | | |||
Db       2255 CCGTAATCATA--TCTTTTTCCTATCTGAGGCACTGGTGGA----------ATAAAAAA 2301

Qy       3149 GCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAG 3207
              |||||||||  ||||||| |||| |||||||||| | || ||||  | ||||| |||  |
Db       2302 CCTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGG 2361

Qy       3208 TGGAGCTGACAGAAATAA 3225
              |||||||   | ||| ||
Db       2362 TGGAGCTAGAAAAAAAAA 2379
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RESULT 15
AAF98399
ID AAF98399 standard; cDNA; 2386 BP.
XX
AC AAF98399;
XX
DT 07-JUN-2001 (first entry)
XX
DE Human cDNA clone BG160_1 sequence SEQ ID 41.
XX
KW Human; secreted protein; nutrient; cytokine modulator; proliferation;
KW differentiation; immune system modulator; tissue growth; chemotactic;
KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
KW haematopoiesis.
XX
OS Homo sapiens.

XX
PN WO200119988-A1.
XX
PD 22-MAR-2001.
XX
PF 14-SEP-2000; 2000WO-US025135.
XX
PR 17-SEP-1999; 99US-00398829.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;
XX
DR WPI; 2001-244801/25.
DR P-PSDB; AAB90682.
XX
PT Isolated nucleic acids encoding polypeptides, useful for modulating e.g.
PT cytokine and cell proliferation/differentiation activity, the immune
PT system and hematopoiesis regulating activity.
XX
PS Claim 1; Page 408-409; 557pp; English.
XX
CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
CC tissue types, and may be used in the prevention, treatment and diagnosis
CC of diseases associated with inappropriate protein expression. The
CC polypeptides and nucleic acids may be used as nutrients or to modulate
CC cytokine and cell proliferation/differentiation activity and may also be
CC involved in modulation of the immune system. The cDNA sequences,
CC proteins, their agonists and/or antagonists exhibit haematopoiesis
CC regulating activity; tissue growth activity; activin/inhibin activity;
CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;
CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis
CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition
CC activity. Included in the invention are probes represented in AAF98490 -
CC AAF98572 which are specific for the cDNA clones encoding the secreted
CC proteins
XX
SQ Sequence 2386 BP; 756 A; 448 C; 496 G; 686 T; 0 U; 0 Other;

Query Match 46.3%; Score 1774; DB 5; Length 2386;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 2099; Conservative 0; Mismatches 260; Indels 59; Gaps 11;

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Db          2 CAAAACATCAAACCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAAC 61

Qy        887 AGATCATGTGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCC 946
              |||| || |  |||||||||| |||||||| ||||||||||||||||||| || || ||
Db         62 AGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCC 121

Qy        947 AGATTTGGTTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGC 1006
              |||||| || |||||||||||||||||||||||||||||| |||||||||||| |||||
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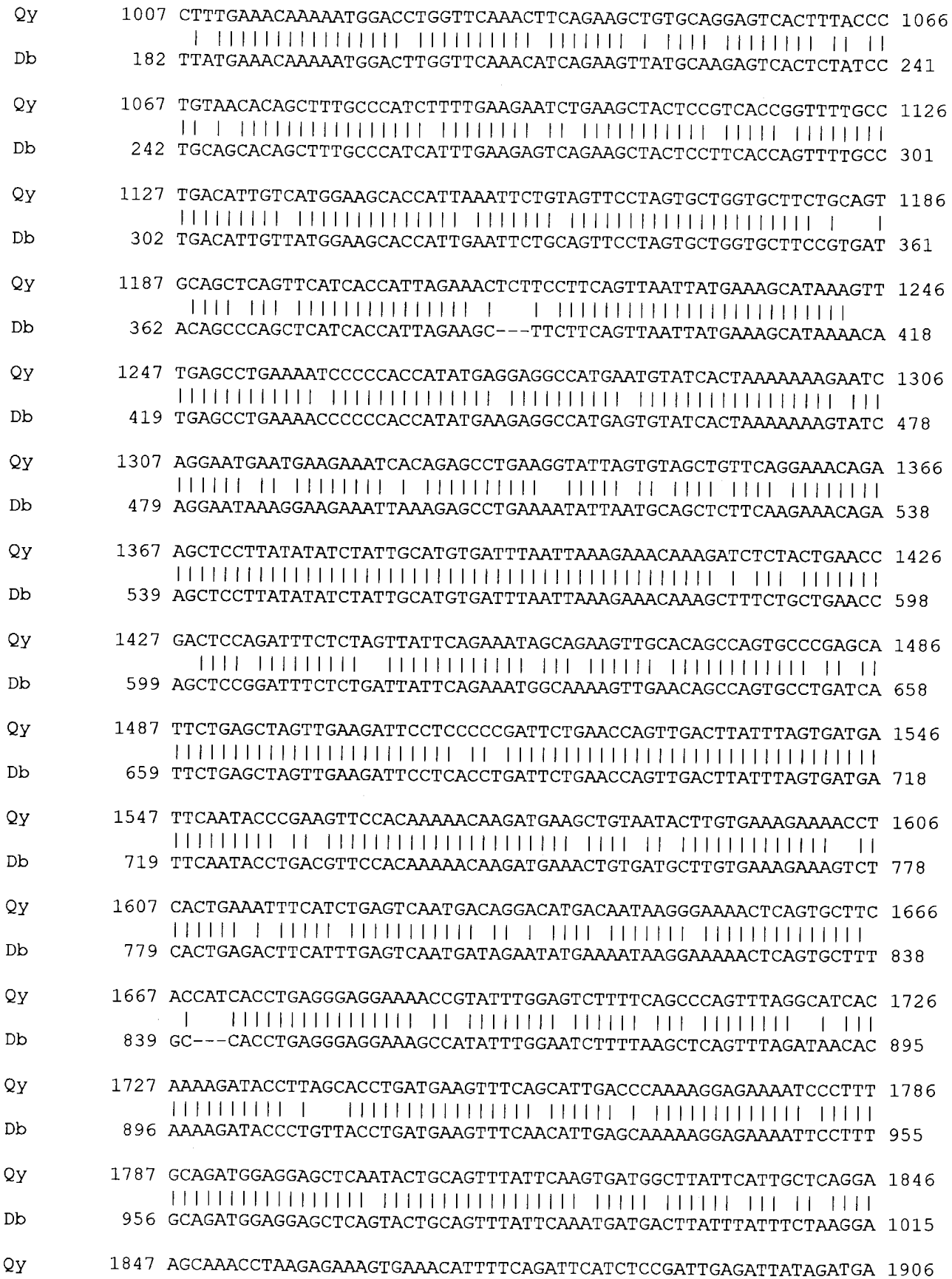

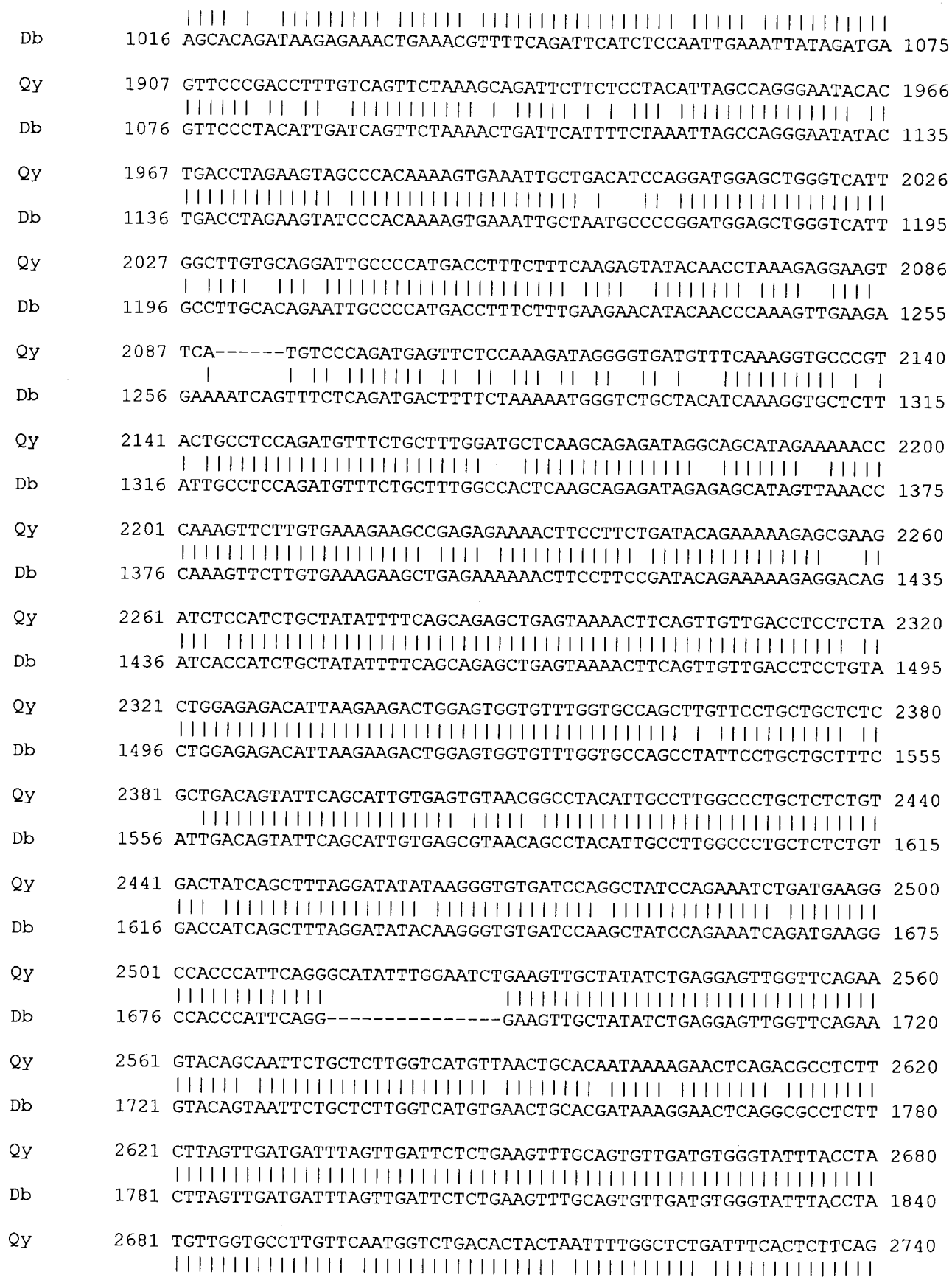

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Qy       2741 TGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAA 2800
              ||||  |||||||||||||||||||||| || |||||||||||||| ||||||||||
Db       1901 TGTTGGTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAA 1960

Qy       2801 TAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAA 2860
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1961 TAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAA 2020

Qy       2861 AGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATAT 2920
              |||||||||| || |||  ||| | |||       ||||||| ||||||||||||||||
Db       2021 AGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATAT 2075

Qy       2921 TCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTT 2980
              ||||||||||  |  |||||||||||||||||| || ||||||| ||||||||||||
Db       2076 TCATTTGATTATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTT 2134

Qy       2981 TCAC-----------AGATCTTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCT 3028
              ||||           |||||||||||||||| | ||| || | |||||||||| ||||
Db       2135 TCACAGATCGTTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCT 2194

Qy       3029 GTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAA 3088
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2195 GTCTTGACTGCCATGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAA 2254

Qy       3089 TCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAA 3148
              ||||||||||  | |||||||| | |||||||||||| |           | | |||
Db       2255 CCGTAATCATA--TCTTTTTCCTATCTGAGGCACTGGTGGA----------ATAAAAAA 2301

Qy       3149 GCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAG 3207
              |||||||||  ||||||| |||| ||||||||| | || ||||  | ||||| |||  |
Db       2302 CCTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGG 2361

Qy       3208 TGGAGCTGACAGAAATAA 3225
              |||||||   | ||| ||
Db       2362 TGGAGCTAGAAAAAAAAA 2379
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(without alignments)
8942.975 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
Sequence: 1 ctatctcctctctcagccgc.....ttaaaaaaaaaaaaaaaaa 3833

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2687.8	70.1	4822	4	US-09-484-970B-106	Sequence 106, App
2	789.8	20.6	2610	4	US-09-023-655-382	Sequence 382, App
3	590.8	15.4	799	2	US-08-700-607-2	Sequence 2, Appli
4	293.4	7.7	536	4	US-09-621-976-3839	Sequence 3839, Ap
5	254.4	6.6	508	4	US-09-621-976-3840	Sequence 3840, Ap
6	230.4	6.0	1766	4	US-09-149-476-254	Sequence 254, App
7	230.4	6.0	2664	4	US-09-149-476-255	Sequence 255, App
8	202.2	5.3	1095	2	US-08-700-607-4	Sequence 4, Appli
9	182	4.7	794	4	US-09-149-476-102	Sequence 102, App
10	174.2	4.5	261	2	US-08-700-607-9	Sequence 9, Appli
11	138.6	3.6	301	4	US-09-439-313-279	Sequence 279, App

	12	138.6	3.6	301	4	US-09-352-616A-279	Sequence 279, App
	13	138.6	3.6	301	4	US-09-232-149A-279	Sequence 279, App
	14	138.6	3.6	301	4	US-09-159-812-279	Sequence 279, App
	15	138.6	3.6	301	4	US-09-636-215-279	Sequence 279, App
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	20	60.8	1.6	200	3	US-09-221-298-100	Sequence 100, App
	21	60.8	1.6	200	4	US-09-401-064-100	Sequence 100, App
	22	46.6	1.2	3095	6	5231168-1	Patent No. 5231168
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	24	44	1.1	1134	3	US-09-248-335-29	Sequence 29, Appl
c	25	43.8	1.1	1949	4	US-08-961-527-289	Sequence 289, App
	26	43.6	1.1	2439	3	US-09-386-493-1	Sequence 1, Appli
c	27	42.8	1.1	949	3	US-08-714-918-12	Sequence 12, Appl
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	39	42.8	1.1	3124	4	US-09-112-580-8	Sequence 8, Appli
c	40	42.8	1.1	6645	4	US-08-956-171E-259	Sequence 259, App
	41	42.4	1.1	2671	6	5168051-9	Patent No. 5168051
	42	42	1.1	277	3	US-09-007-005-3	Sequence 3, Appli
	43	42	1.1	277	3	US-09-244-796-3	Sequence 3, Appli
	44	41.6	1.1	21234	4	US-09-810-671-3	Sequence 3, Appli
	45	41.6	1.1	21234	4	US-10-109-854-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-09-484-970B-106
; Sequence 106, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
;  APPLICANT:  Jones, Karen A.
;  APPLICANT:  Volkmuth, Wayne
;  APPLICANT:  Walker, Michael G.
;  TITLE OF INVENTION:  BONE REMODELING GENES
;  FILE REFERENCE:  PB-0014 US
;  CURRENT APPLICATION NUMBER: US/09/484,970B
;  CURRENT FILING DATE:  2000-01-18
;  NUMBER OF SEQ ID NOS:  172
;  SOFTWARE:  PERL Program
; SEQ ID NO 106
;   LENGTH: 4822
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
; NAME/KEY: unsure
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-106

Query Match 70.1%; Score 2687.8; DB 4; Length 4822;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 3333; Conservative 0; Mismatches 458; Indels 104; Gaps 27;

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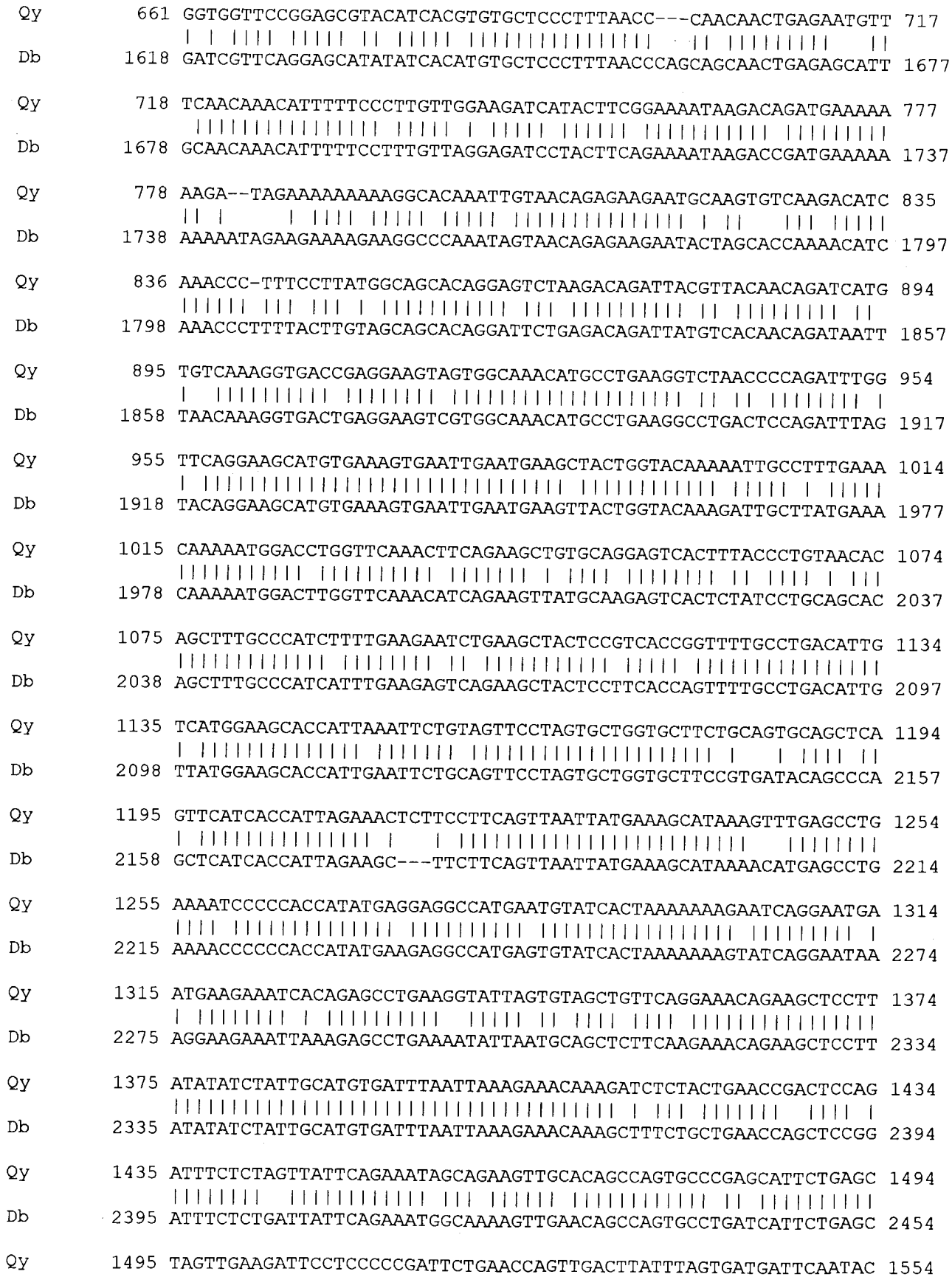
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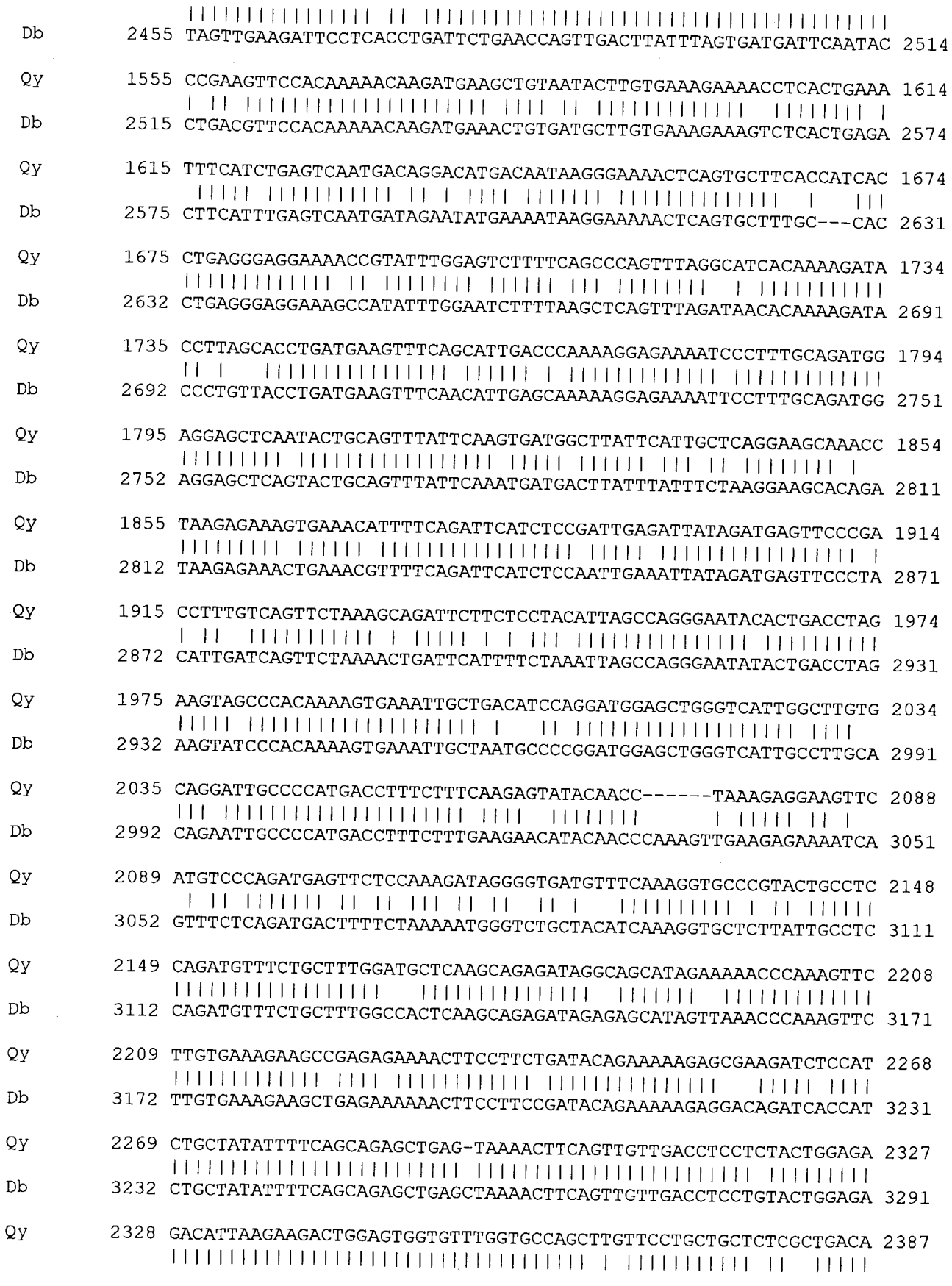

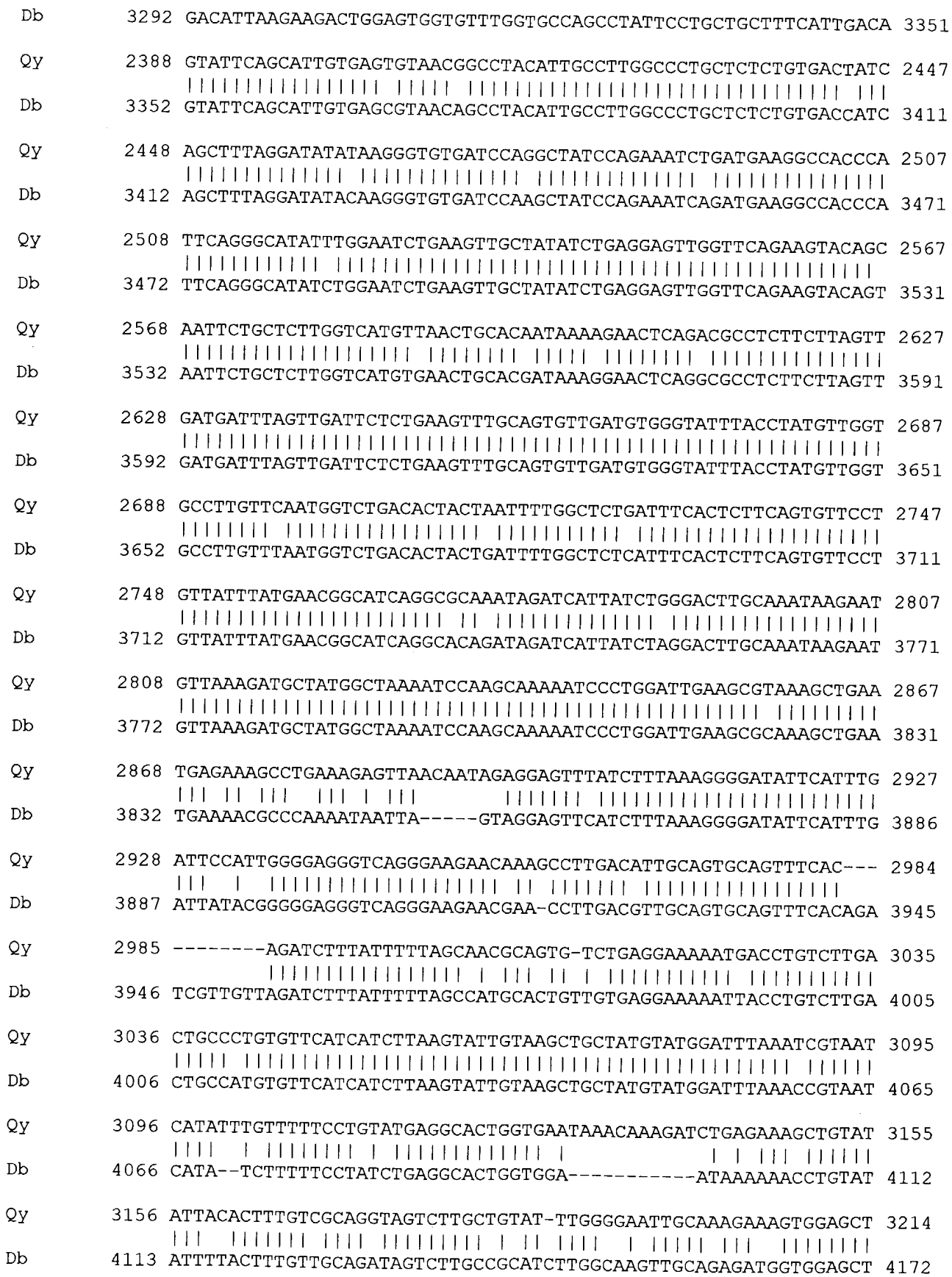

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Db       4293 ATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATT 4351

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Db       4352 AATTGCCAATATAAGTAAATATAGATTATATATG------TATAGTGTTTCACAAAGCTT 4405

Qy       3443 AGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT------TCTGTCATGGGTTT 3496
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Qy       3497 TATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCA 3556
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Qy       3557 TCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTG 3615
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RESULT 2
US-09-023-655-382
; Sequence 382, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508

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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  382:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2610 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
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;      CLONE:  1508778
US-09-023-655-382

  Query Match             20.6%;  Score 789.8;  DB 4;  Length 2610;
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Qy       2483 CCAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATC 2542
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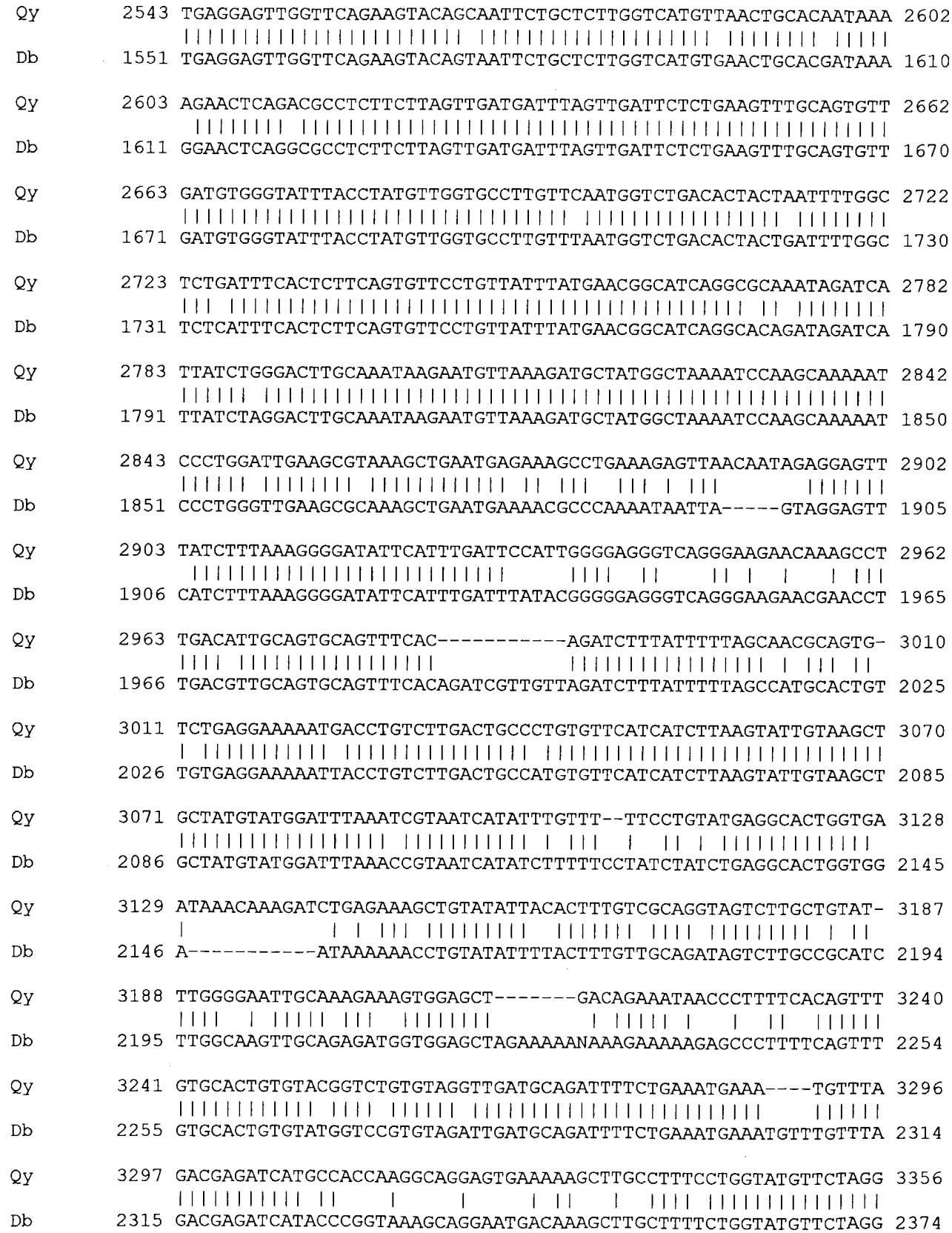

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Qy       3417 TCTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTT 3476
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Db       2489 GATAATTC 2496
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RESULT 3
US-08-700-607-2
; Sequence 2, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-700-607-2

Query Match 15.4%; Score 590.8; DB 2; Length 799;
Best Local Similarity 92.9%; Pred. No. 7e-140;
Matches 643; Conservative 0; Mismatches 42; Indels 7; Gaps 2;

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Qy       2364 TTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
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Qy       2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
             ||||||||||||||||||| ||||||||||||||||  ||||||||||||||  ||||||
Db        228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 287

Qy       2484 CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
             ||||||||  ||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        288 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 347

Qy       2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAA 2603
             ||||||||||||||||||||||  ||||||||||||||||||  ||||||||  |||||
Db        348 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 407

Qy       2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 2663
             ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 467

Qy       2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT 2723
             ||||||||||||||||||||||||||||||||  ||||||||||||||||  |||||||||
Db        468 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 527

Qy       2724 CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
             ||  ||||||||||||||||||||||||||||||||||||||||||  ||  |||||||||
Db        528 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 587

Qy       2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
             |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 647

Qy       2844 CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT 2903
             |||||||||||||| ||||||||||| ||  |||  |||  |  |||        |||||||
Db        648 CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTC 702

Qy       2904 ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTT 2963
             |||||||||||||||||||||||||||  |  ||||||||||||||||||||  |  ||||
Db        703 ATCTTTAAAGGGGATATTCATTTGATTATACGGGGGAGGGTCAGGGAAGAACGA--CCTT 760

Qy       2964 GACATTGCAGTGCAGTTTCACAGATCTTTATT 2995
              ||| ||||||||||||||||||||| ||  ||
Db        761 GACGTTGCAGTGCAGTTTCACAGATCGTTGTT 792
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RESULT 4
US-09-621-976-3839
; Sequence 3839, Application US/09621976

; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3839
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..224
US-09-621-976-3839

Query Match 7.7%; Score 293.4; DB 4; Length 536;
Best Local Similarity 82.8%; Pred. No. 1.1e-64;
Matches 443; Conservative 0; Mismatches 56; Indels 36; Gaps 8;

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Qy       3291 TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGT 3350
             ||||||||||||||||||  ||   || ||||||  ||| |||||||||  ||| |||||||||
Db         13 TGTTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTGCTTTT-CTGGTATGT 71

Qy       3351 TCTAGGTGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTA 3410
             ||||||||||||||||  |||||||||  ||||||||||||||||||||||||||||||||
Db         72 TCTAGGTGTATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGTAAATATAGATTA 131

Qy       3411 TATATATCTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACA 3470
             ||      ||| ||||||||||||| ||||||||  |||||||||  |||||  |||||||
Db        132 TA------TATGTATAGTGTTTCACAAAGCTTAGACCTTTACCTT-CCAGCCACCCCACA 184

Qy       3471 GTGCTTGATACT------TCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGC 3524
             ||||||||||  |      ||  |||||  ||||  ||  ||||||||  ||||||||||||||
Db        185 GTGCTTGATATTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCAAAGCACATAAGC 244

Qy       3525 TAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATG 3584
             |||    | |  ||  |||||||  ||||||||||||||||||||||  |||  | |
Db        245 TAGAAGAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAACATGAAATGCC-----A 299

Qy       3585 CAAACAGAACTCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCAC 3644
             ||  |||  |   |  ||||||  ||  ||||  ||||||||||  ||||||||||||||  ||||
Db        300 CACACATAGAACTCCAACATCAATTTCATTGCACAGACTGACTGTAGTTAATTTTGTCAC 359

Qy       3645 --AAACTCTGGACTGAATCTAATGCTTCCAAAAATGTT-------TGCAAATATCAAACA 3695
                ||  ||  ||||||||||||||||||||||||||||||       |||||||||||||||
Db        360 AGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTTTGCAAATATCAAACA 419

Qy       3696 TTGTTATGTAAGAAAATAT--------AAATGACGATTTATACAATTGTGGTTTAAGCTG 3747
             ||||||||  ||||||  |||         ||||||  |||||||||  ||||||||||||||||
Db        420 TTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACCATTGTGGTTTAAGCTG 479

Qy       3748 TATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAA 3802
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Db        480 TACTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAA 534


RESULT 5
US-09-621-976-3840
; Sequence 3840, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 3840
;   LENGTH: 508
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 3..224
US-09-621-976-3840

  Query Match             6.6%;  Score 254.4;  DB 4;  Length 508;
  Best Local Similarity   81.5%;  Pred. No. 8.2e-55;
  Matches  404;  Conservative    0;  Mismatches   56;  Indels   36;  Gaps    8;

Qy       3291 TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGT 3350
              |||||||||||||||||| ||   || |||||| ||| ||||||||| ||| |||||||||
Db         13 TGTTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTGCTTTT-CTGGTATGT 71

Qy       3351 TCTAGGTGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTA 3410
              ||||||||||||||||  ||||||||| ||||||||||||||||||||||||||||||||
Db         72 TCTAGGTGTATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGTAAATATAGATTA 131

Qy       3411 TATATATCTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACA 3470
              ||      ||| |||||||||||| |||||||| |||||||||| |||||  |||||||
Db        132 TA------TATGTATAGTGTTTCACAAAGCTTAGACCTTTACCTT-CCAGCCACCCCACA 184

Qy       3471 GTGCTTGATACT------TCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGC 3524
              |||||||||| |      || ||||| |||| ||  |||||||| ||||||||||||||
Db        185 GTGCTTGATATTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCAAAGCACATAAGC 244

Qy       3525 TAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATG 3584
              |||    | |  || ||||||| |||||||||||||||||||||| |||  | |
Db        245 TAGAAGAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAACATGAAATGCC-----A 299

Qy       3585 CAAACAGAACTCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCAC 3644
              || ||| |   |  |||||| || |||| |||||||||| |||||||||||||| ||||
Db        300 CACACATAGAACTCCAACATCAATTTCATTGCACAGACTGACTGTAGTTAATTTTGTCAC 359

Qy       3645 --AAACTCTGGACTGAATCTAATGCTTCCAAAAA-------TGTTTGCAAATATCAAACA 3695
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Db        360 AGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTTTGCAAATATCAAACA 419

Qy       3696 TTGTTATGTAAGAAAATAT--------AAATGACGATTTATACAATTGTGGTTTAAGCTG 3747
              |||||||| |||||| |||         |||||| ||||||||| ||||||||||||||||
Db        420 TTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACCATTGTGGTTTAAGCTG 479

Qy       3748 TATTGAACTAAATCTG 3763
              || ||||||||||||||
Db        480 TACTGAACTAAATCTG 495
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RESULT 6
US-09-149-476-254
; Sequence 254, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893

; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 6.0%; Score 230.4; DB 4; Length 1766;
Best Local Similarity 63.6%; Pred. No. 1.8e-48;
Matches 351; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

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Db        406 CATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGC 465

Qy       2480 TATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTAT 2539
              | | ||||| || || |||||||| ||||||| || || |||| || || || | |
Db        466 TGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCT 525

Qy       2540 ATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAAT 2599
               ||    ||     | || || |||| ||| |||| | | || | ||| | | |
Db        526 GTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCT 585

Qy       2600 AAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGT 2659
               |||    | |  || |||||  | || || ||| | ||||| ||  ||||| | || ||
Db        586 GAAACTCATTATTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGT 645

Qy       2660 GTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTT 2719
               || |||||| |  | ||||||||||||||  | || || ||  | || || |||||| |
Db        646 CTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCT 705

Qy       2720 GGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGA 2779
               |||    |     | |||||||| ||  || | |||||   | |  || | || || ||
Db        706 TGCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGA 765

Qy       2780 TCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAA 2839
              ||| ||| | ||  | ||     |  |    ||      | | |  || ||||||||||
Db        766 TCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAA 825

Qy       2840 AATCCCTGGATT 2851
              | |||||||| |
Db        826 ACTCCCTGGAAT 837
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RESULT 7
US-09-149-476-255
; Sequence 255, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,333
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/038,621
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,626
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,334
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,336
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,163
;  EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
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; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/057,650
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; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 6.0%; Score 230.4; DB 4; Length 2664;
Best Local Similarity 63.6%; Pred. No. 2.2e-48;
Matches 351; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

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Qy       2480 TATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTAT 2539
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RESULT 8
US-08-700-607-4
; Sequence 4, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
;   APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: THP1NOB01
; CLONE: 31870
US-08-700-607-4

Query Match 5.3%; Score 202.2; DB 2; Length 1095;
Best Local Similarity 63.7%; Pred. No. 1.9e-41;
Matches 303; Conservative 1; Mismatches 172; Indels 0; Gaps 0;

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; Sequence 102, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 4.7%; Score 182; DB 4; Length 794;
Best Local Similarity 61.2%; Pred. No. 2.2e-36;
Matches 333; Conservative 6; Mismatches 201; Indels 4; Gaps 3;

Qy 2300 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGC 2359

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Db        253 TGCGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTG--GA 310

Qy       2360 CAGCTTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCC-TACA 2418
              ||   || || ||||||| || ||| |||  |||||  |  | |:|||      | ||:
Db        311 CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCARTGTGGGTTTCTTAMC 370

Qy       2419 TTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGG 2478
              |   | |||| || |||||||| || ||||:||| ||||| || |||   || ||||| |
Db        371 TCATCCTGGCTCTTCTCTCTGTCACCATCARCTTCAGGATCTACAAGTCCGTCATCCAAG 430

Qy       2479 CTATCCAGAAATCTGATGAAGGCCACCCATT-CAGGGCATATTTGGAATCTGAAGTTGCT 2537
              || | |||||:|| || :|||||||| |||:| ||  || ||  |||| || || ||
Db        431 CTGTWCAGAARTCAGAARAAGGCCATCCAWTCCAAAGCCTACCTGGACGTAGACATTACT 490

Qy       2538 ATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACA 2597
               | ||    ||     | || || ||||  ||| ||||  | |  ||  | ||| |  |
Db        491 CTGTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCC 550

Qy       2598 ATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCA 2657
               | |||    | |  || |||||  | || || ||| | ||||| ||  ||||| | ||
Db        551 CTGAAACTCATTATTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCT 610

Qy       2658 GTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATT 2717
              || || |||||| |  | ||||||||||||||  | || || ||  | || || ||||||
Db        611 GTCTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATT 670

Qy       2718 TTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATA 2777
               | |||    |     | |||||||| ||  || | |||||   | |  || | || ||
Db        671 CTTGCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATT 730

Qy       2778 GATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCA 2837
              ||||| ||| | ||  | ||     |  |    ||      | | |  || |||| |
Db        731 GATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGC 790

Qy       2838 AAAA 2841
              ||||
Db        791 AAAA 794
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RESULT 10
US-08-700-607-9
; Sequence 9, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: SPLNFET01
; CLONE: 28742
US-08-700-607-9

Query Match 4.5%; Score 174.2; DB 2; Length 261;
Best Local Similarity 89.7%; Pred. No. 1.2e-34;
Matches 182; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Qy       2363 CTTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGC 2422
              | | | || |||||| ||  |||||||||||||||||||||| ||||| ||||||||||
Db          1 CCTATNCCNGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGC 60

Qy       2423 CTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTAT 2482
              ||| ||||||| ||||||||| ||||||| |||| |||| |||||||||||||| |||||
Db         61 CTTNGCCCTGCNCTCTGTGACCATCAGCTNTAGGCTATACAAGGGTGTGATCCAAGCTAT 120

Qy       2483 CCAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATC 2542
              ||||||||| |||||||| |||||||||||||||||| |||| ||||||||||||||||
Db        121 CCAGAAATCAGATGAAGGNCACCCATTCAGGGCATATCTGGANTCTGAAGTTGCTATATC 180

Qy       2543 TGAGGAGTTGGTTCAGAAGTACA 2565
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Db        181 TGAGGAGTTGNTTCAGAAGTACA 203
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RESULT 11
US-09-439-313-279
; Sequence 279, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise

```
;  APPLICANT:  Jiang Yuqui
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Kalos, Michael
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Retter, Mark
;  APPLICANT:  Solk, John
;  APPLICANT:  Day, Craig
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C9
;  CURRENT APPLICATION NUMBER: US/09/439,313
;  CURRENT FILING DATE:  1999-11-12
;  NUMBER OF SEQ ID NOS: 575
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 279
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(301)
;   OTHER INFORMATION: n = A,T,C or G
US-09-439-313-279

  Query Match             3.6%;  Score 138.6;  DB 4;  Length 301;
  Best Local Similarity   80.3%;  Pred. No. 1.3e-25;
  Matches  253;  Conservative    0;  Mismatches   41;  Indels   21;  Gaps    7;

Qy       3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 3373
              || |||||| ||| |||||||| |||| |||||||||||||||||||||||  |||||
Db             1 AAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTAC 59

Qy       3374 TGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTC 3433
              |||| ||||||||||||||||||||||||||||||||      ||| ||||||||||
Db            60 TGTTATATTAATTGCCAATATAAGTAAATATAGATTATA------TATGTATAGTGTTTC 113

Qy       3434 ACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT------TCTGT 3487
              || |||||||| |||||||||| |||||  |||||||||||||||| |      || ||
Db           114 ACAAAGCTTAGACCTTTACCTT-CCAGCCACCCCACAGTGCTTGATATTTCAGAGTCAGT 172

Qy       3488 CATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTA-GG 3546
              ||| |||| ||  |||||||| ||||||||||||||||    | |  || ||||| ||
Db           173 CATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAANAANAAATATTTCTAGGG 232

Qy       3547 CGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCAACATAA 3606
               ||||||||||||||||||     |    | ||||  || | |||||||  |||||| |
Db           233 AGCACTACCATCTGTTTTCA----CATGAAATGCCACACACATAGAACTC--CAACATCA 286

Qy       3607 ACTTCACTGCACAGA 3621
              | |||| ||||||||
Db           287 ATTTCATTGCACAGA 301


RESULT 12
US-09-352-616A-279
; Sequence 279, Application US/09352616A
; Patent No. 6395278
```

; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 279
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(301)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-279

Query Match 3.6%; Score 138.6; DB 4; Length 301;
Best Local Similarity 80.3%; Pred. No. 1.3e-25;
Matches 253; Conservative 0; Mismatches 41; Indels 21; Gaps 7;

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Qy       3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 3373
              || |||||| ||| |||||||| |||| |||||||||||||||||||||||  |||||
Db             1 AAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTAC 59

Qy       3374 TGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTC 3433
              |||| |||||||||||||||||||||||||||||||||      ||| ||||||||||
Db            60 TGTTATATTAATTGCCAATATAAGTAAATATAGATTATA------TATGTATAGTGTTTC 113

Qy       3434 ACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT------TCTGT 3487
              || |||||||| |||||||||| |||||  |||||||||||||||| |      || ||
Db           114 ACAAAGCTTAGACCTTTACCTT-CCAGCCACCCCACAGTGCTTGATATTTCAGAGTCAGT 172

Qy       3488 CATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTA-GG 3546
              ||| |||| ||  |||||||| ||||||||||||||||    | |  || ||||| ||
Db           173 CATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAANAANAAATATTTCTAGGG 232

Qy       3547 CGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCAACATAA 3606
               ||||||||||||||||||     |    | ||||  || | |||||||  |||||| |
Db           233 AGCACTACCATCTGTTTTCA----CATGAAATGCCACACACATAGAACTC--CAACATCA 286

Qy       3607 ACTTCACTGCACAGA 3621
              | |||| ||||||||
Db           287 ATTTCATTGCACAGA 301
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RESULT 13
US-09-232-149A-279
; Sequence 279, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:

```
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer Lynn
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
;  TITLE OF INVENTION:  CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.427C6
;  CURRENT APPLICATION NUMBER: US/09/232,149A
;  CURRENT FILING DATE:  1999-01-15
;  NUMBER OF SEQ ID NOS: 338
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 279
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(301)
;   OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-279

  Query Match             3.6%;  Score 138.6;  DB 4;  Length 301;
  Best Local Similarity   80.3%;  Pred. No. 1.3e-25;
  Matches  253;  Conservative    0;  Mismatches   41;  Indels   21;  Gaps    7;

Qy       3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 3373
              || |||||| ||| |||||||| |||| |||||||||||||||||||||||||  |||||
Db             1 AAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTAC 59

Qy       3374 TGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTC 3433
              |||| ||||||||||||||||||||||||||||||||      ||| ||||||||||
Db            60 TGTTATATTAATTGCCAATATAAGTAAATATAGATTATA------TATGTATAGTGTTTC 113

Qy       3434 ACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT------TCTGT 3487
              || |||||||| |||||||||| |||||  |||||||||||||||| |      || ||
Db           114 ACAAAGCTTAGACCTTTACCTT-CCAGCCACCCCACAGTGCTTGATATTTCAGAGTCAGT 172

Qy       3488 CATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTA-GG 3546
              ||| |||| ||  |||||||| ||||||||||||||||||    | |  || ||||| ||
Db           173 CATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAANAANAAATATTTCTAGGG 232

Qy       3547 CGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCAACATAA 3606
              ||||||||||||||||||     |    | ||||  || | |||||||  |||||| |
Db           233 AGCACTACCATCTGTTTTCA----CATGAAATGCCACACACATAGAACTC--CAACATCA 286

Qy       3607 ACTTCACTGCACAGA 3621
              | |||| ||||||||
Db           287 ATTTCATTGCACAGA 301


RESULT 14
US-09-159-812-279
; Sequence 279, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT: Dillon, Davin C.
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
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;  TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.428C5
;  CURRENT APPLICATION NUMBER: US/09/159,812A
;  CURRENT FILING DATE: 1998-09-23
;  NUMBER OF SEQ ID NOS: 306
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 279
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(301)
;   OTHER INFORMATION: n = A,T,C or G
US-09-159-812-279

  Query Match             3.6%;  Score 138.6;  DB 4;  Length 301;
  Best Local Similarity   80.3%;  Pred. No. 1.3e-25;
  Matches  253;  Conservative    0;  Mismatches   41;  Indels   21;  Gaps    7;

Qy       3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 3373
              || |||||| ||| |||||||| |||| |||||||||||||||||||||||  |||||
Db             1 AAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTAC 59

Qy       3374 TGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTC 3433
              |||| |||||||||||||||||||||||||||||||      ||| ||||||||||
Db            60 TGTTATATTAATTGCCAATATAAGTAAATATAGATTATA------TATGTATAGTGTTTC 113

Qy       3434 ACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT------TCTGT 3487
              || |||||||| |||||||||| |||||  |||||||||||||||| |      || ||
Db           114 ACAAAGCTTAGACCTTTACCTT-CCAGCCACCCCACAGTGCTTGATATTTCAGAGTCAGT 172

Qy       3488 CATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTA-GG 3546
              ||| |||| ||  |||||||| ||||||||||||||||    | |  || ||||| ||
Db           173 CATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAANAANAAATATTTCTAGGG 232

Qy       3547 CGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCAACATAA 3606
              ||||||||||||||||||     |    | ||||  || | |||||||  |||||| |
Db           233 AGCACTACCATCTGTTTTCA----CATGAAATGCCACACACATAGAACTC--CAACATCA 286

Qy       3607 ACTTCACTGCACAGA 3621
              | |||| ||||||||
Db           287 ATTTCATTGCACAGA 301


RESULT 15
US-09-636-215-279
; Sequence 279, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
```

```
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42717C17
;  CURRENT APPLICATION NUMBER: US/09/636,215
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS:  852
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 279
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(301)
;   OTHER INFORMATION: n = A,T,C or G
US-09-636-215-279

  Query Match             3.6%;  Score 138.6;  DB 4;  Length 301;
  Best Local Similarity   80.3%;  Pred. No. 1.3e-25;
  Matches  253;  Conservative    0;  Mismatches   41;  Indels   21;  Gaps    7;

Qy       3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 3373
              || |||||| ||| |||||||| |||| ||||||||||||||||||||||||  |||||
Db             1 AAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTAC 59

Qy       3374 TGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTC 3433
              |||| ||||||||||||||||||||||||||||||||      ||| ||||||||||
Db            60 TGTTATATTAATTGCCAATATAAGTAAATATAGATTATA------TATGTATAGTGTTTC 113

Qy       3434 ACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT------TCTGT 3487
              || |||||||| |||||||||| |||||  |||||||||||||||| |      || ||
Db           114 ACAAAGCTTAGACCTTTACCTT-CCAGCCACCCCACAGTGCTTGATATTTCAGAGTCAGT 172

Qy       3488 CATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTA-GG 3546
              ||| |||| ||  |||||||| ||||||||||||||||    | |  || ||||| ||
Db           173 CATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAANAANAAATATTTCTAGGG 232

Qy       3547 CGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCAACATAA 3606
               ||||||||||||||||||     |    | ||||  || | |||||||  |||||| |
Db           233 AGCACTACCATCTGTTTTCA----CATGAAATGCCACACACATAGAACTC--CAACATCA 286

Qy       3607 ACTTCACTGCACAGA 3621
              | |||| ||||||||
Db           287 ATTTCATTGCACAGA 301


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OM nucleic - nucleic search, using sw model

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(without alignments)
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Perfect score: 3833
Sequence: 1 ctatctcctctctcagccgc.....ttaaaaaaaaaaaaaaaaa 3833

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query

	No.	Score	Match	Length	DB	ID	Description
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	2	2379.4	62.1	4053	9	US-09-758-140-5	Sequence 5, Appli
	3	2379.4	62.1	4053	9	US-09-972-599A-5	Sequence 5, Appli
	4	2379.4	62.1	4053	17	US-10-717-597-310	Sequence 310, App
	5	2223.6	58.0	3579	9	US-09-789-386-1	Sequence 1, Appli
	6	2223.6	58.0	3579	9	US-09-893-348-22	Sequence 22, Appl
	7	2223.6	58.0	3579	12	US-10-267-502-212	Sequence 212, App
	8	2223.6	58.0	3579	17	US-10-327-213-8	Sequence 8, Appli
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	15	986	25.7	1798	17	US-10-466-258-10	Sequence 10, Appl
	16	915.6	23.9	1785	16	US-10-439-388-62	Sequence 62, Appl
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	18	826.4	21.6	2782	15	US-10-205-194-165	Sequence 165, App
	19	789.8	20.6	2610	17	US-10-641-643-382	Sequence 382, App
	20	685.8	17.9	1610	9	US-09-765-205-5	Sequence 5, Appli
	21	683	17.8	1160	15	US-10-175-523-156	Sequence 156, App
	22	681.4	17.8	994	12	US-09-978-360A-110	Sequence 110, App
	23	590.8	15.4	799	13	US-10-660-946-2	Sequence 2, Appli
	24	538.8	14.1	868	9	US-09-789-386-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 53, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 4632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-53

Query Match 69.1%; Score 2649.8; DB 15; Length 4632;
Best Local Similarity 85.0%; Pred. No. 0;
Matches 3292; Conservative 0; Mismatches 442; Indels 137; Gaps 24;

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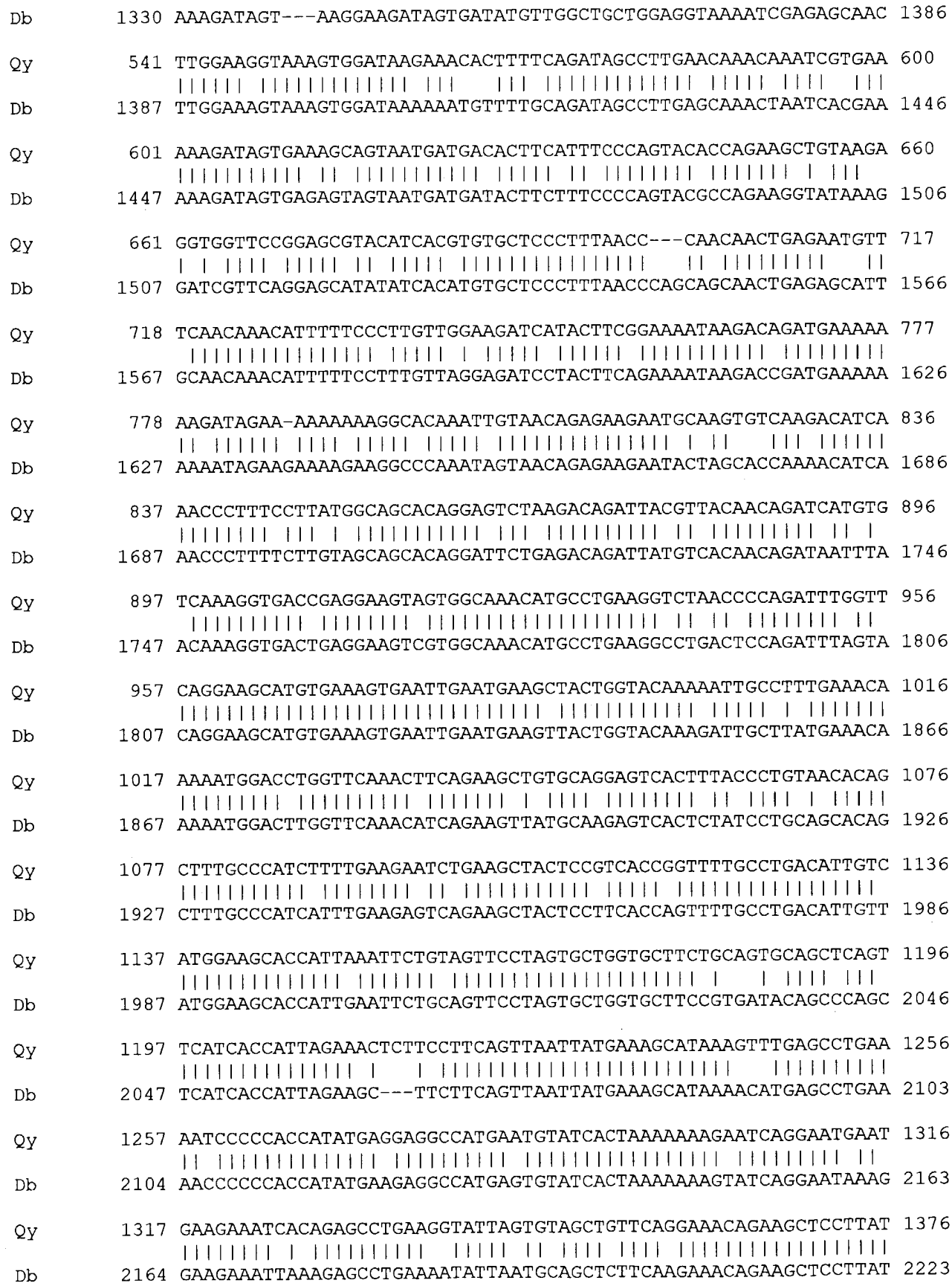

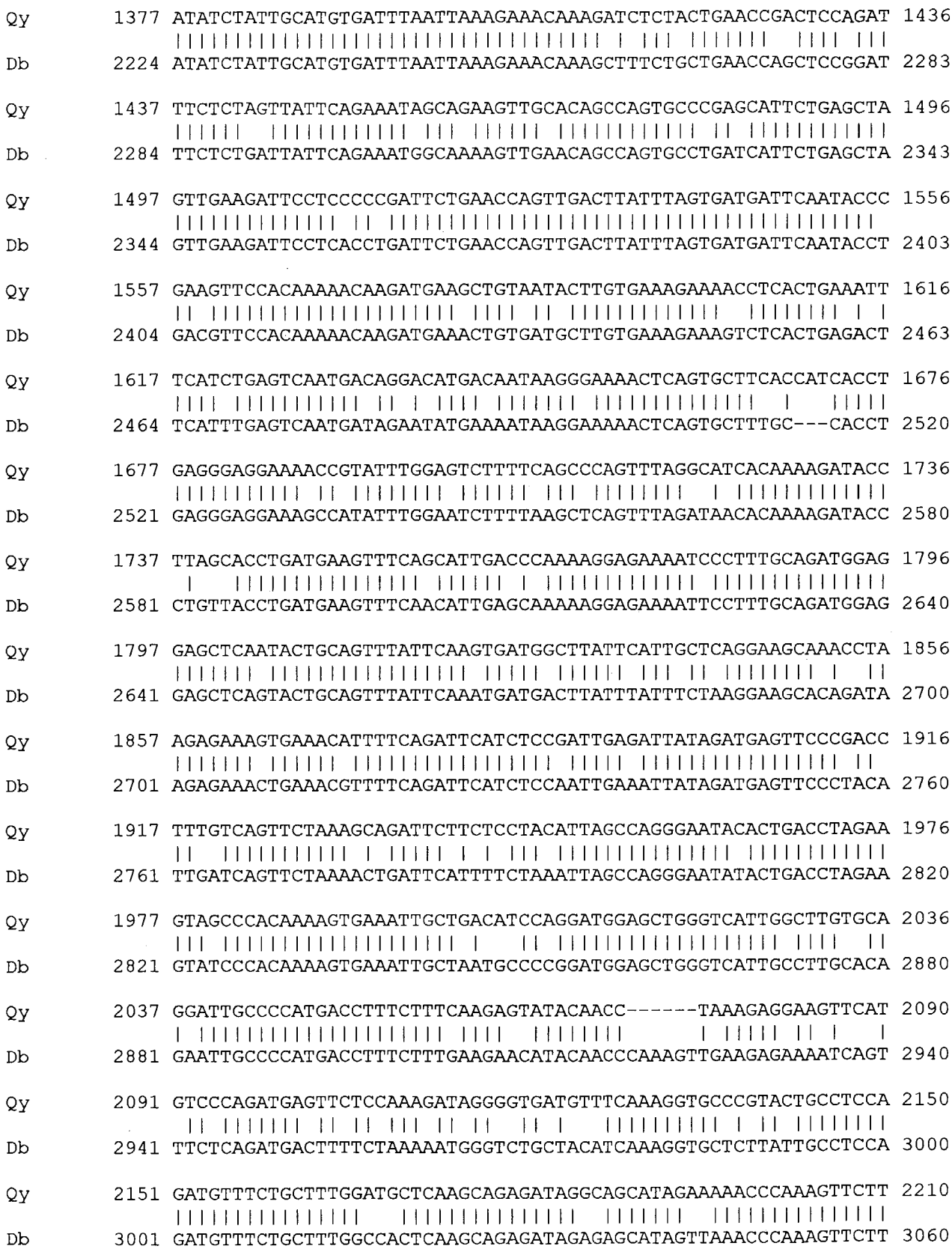

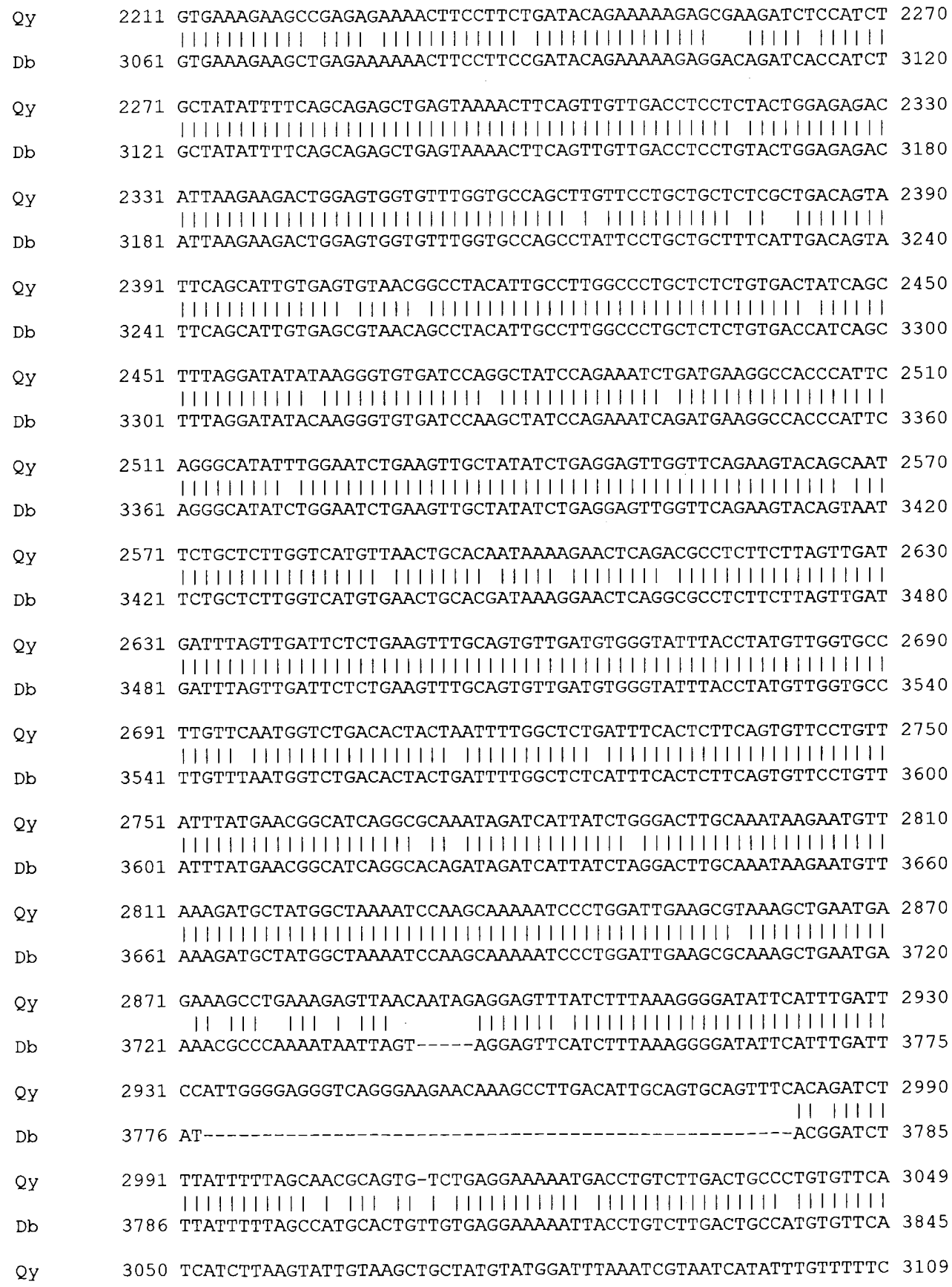

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RESULT 2

US-09-758-140-5
; Sequence 5, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(3710)
; OTHER INFORMATION: Human mRNA for No. US20020012965A1o protein (KIAA0886, GenBank
; OTHER INFORMATION: Accession No. US20020012965A1 AB020693)
US-09-758-140-5

Query Match 62.1%; Score 2379.4; DB 9; Length 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

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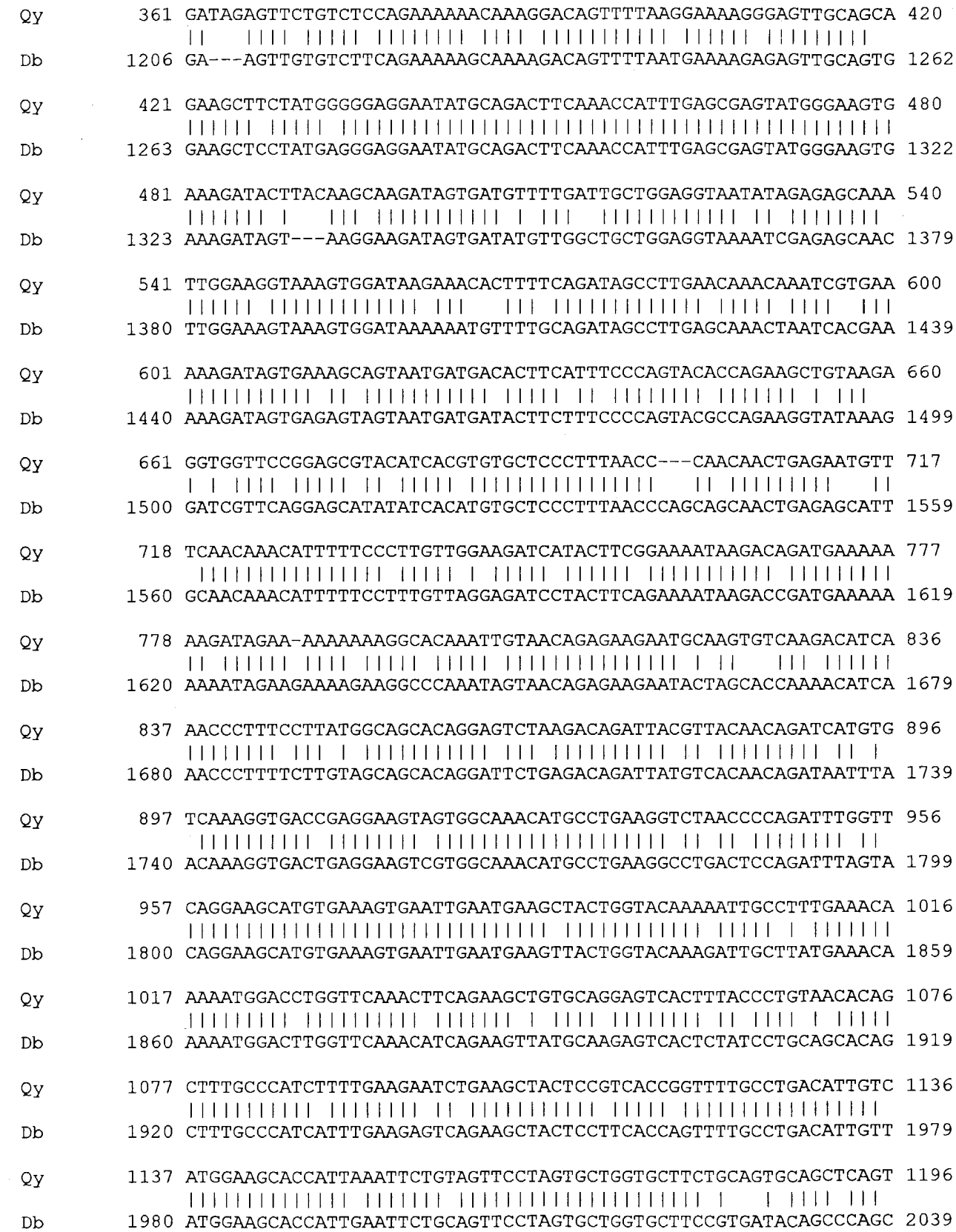

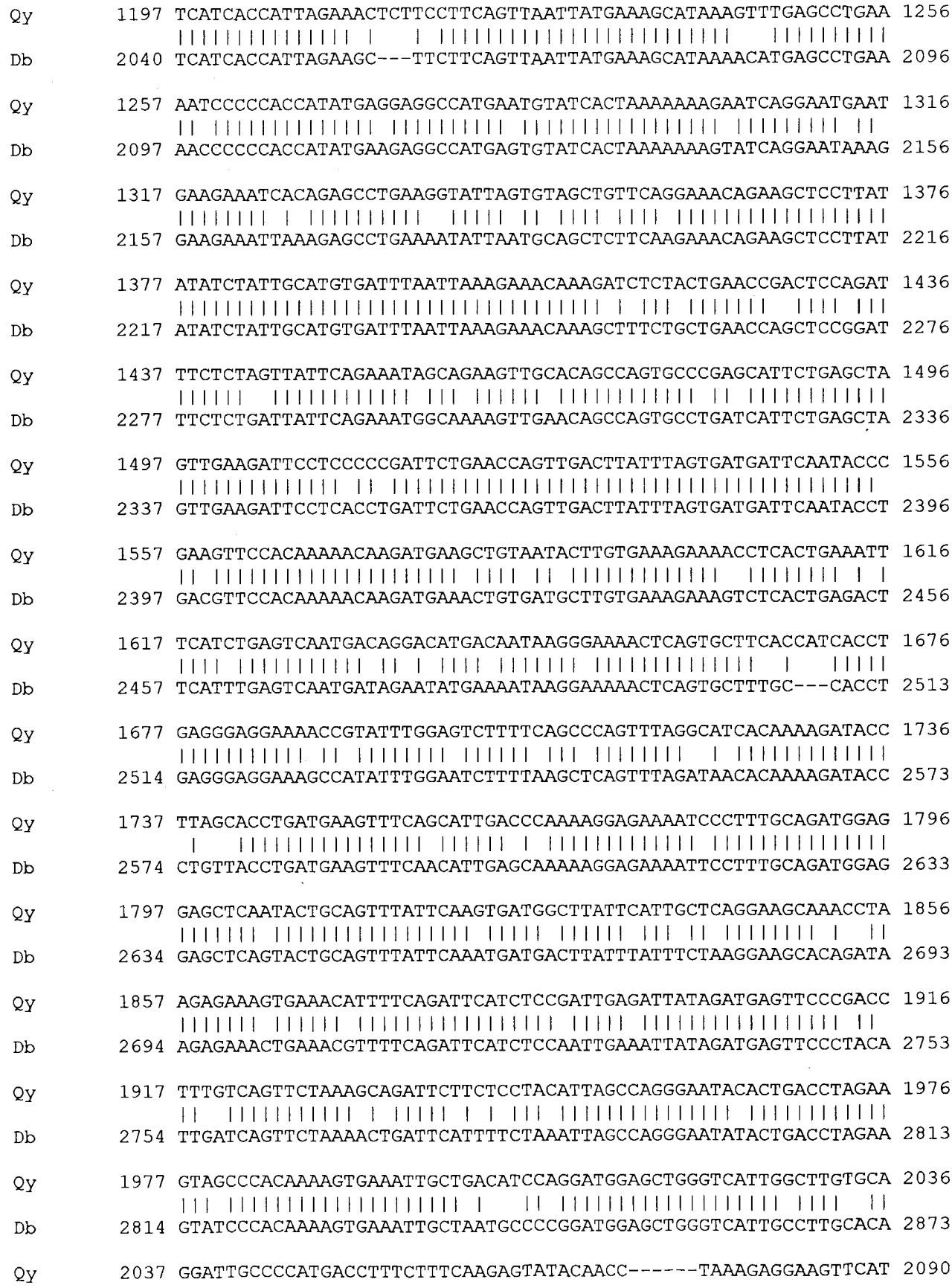

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RESULT 3
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; Sequence 5, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
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; NAME/KEY: CDS
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; OTHER INFORMATION: Human DNA encoding for No. US20020077295A1o protein
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; OTHER INFORMATION: Accession No. US20020077295A1 AB020693)
US-09-972-599A-5

Query Match 62.1%; Score 2379.4; DB 9; Length 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

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Db       1263 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1322

Qy        481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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Qy        601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
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Qy        661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGTT 717
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Qy        718 TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
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Db       1560 GCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA 1619

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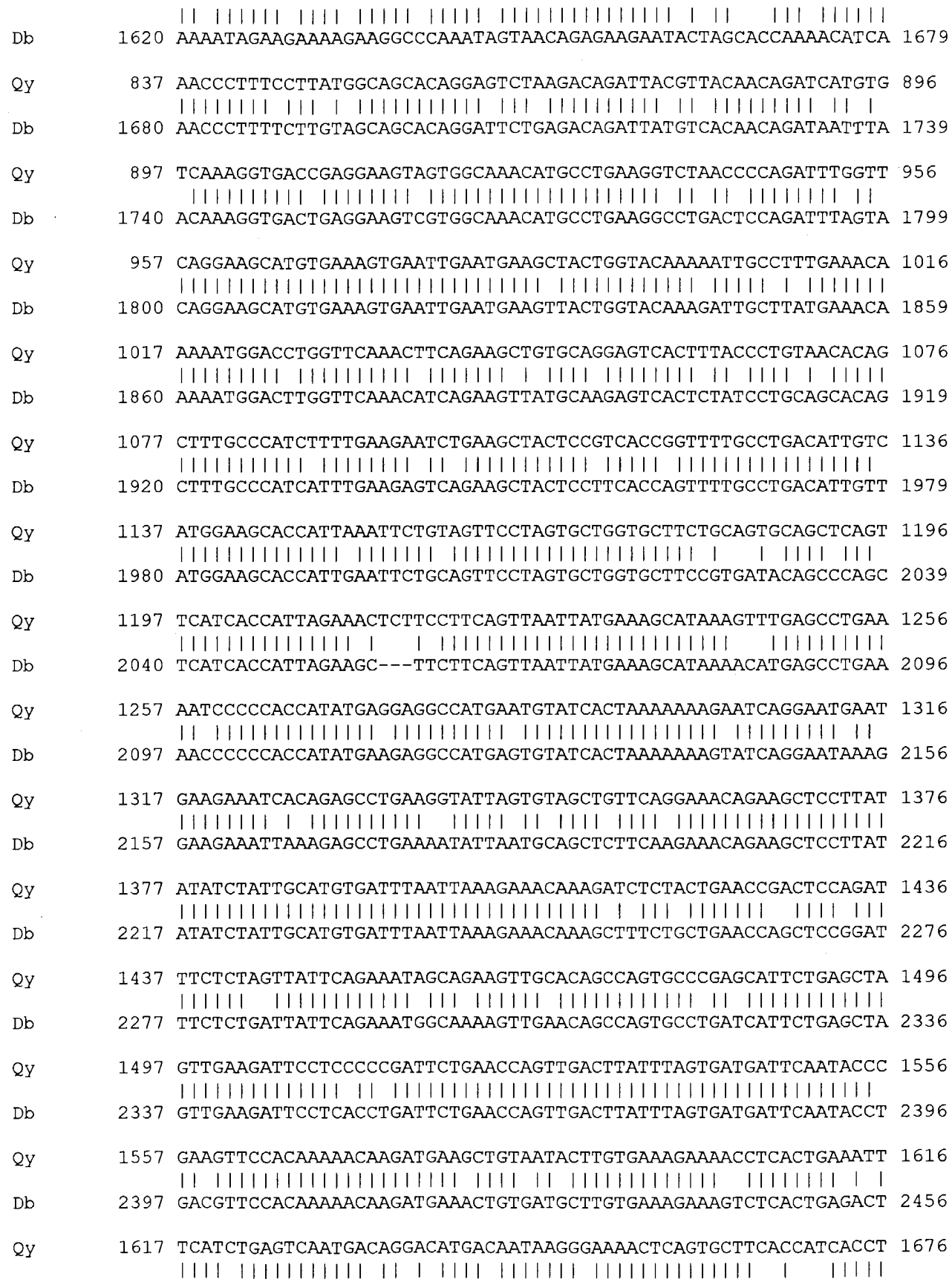

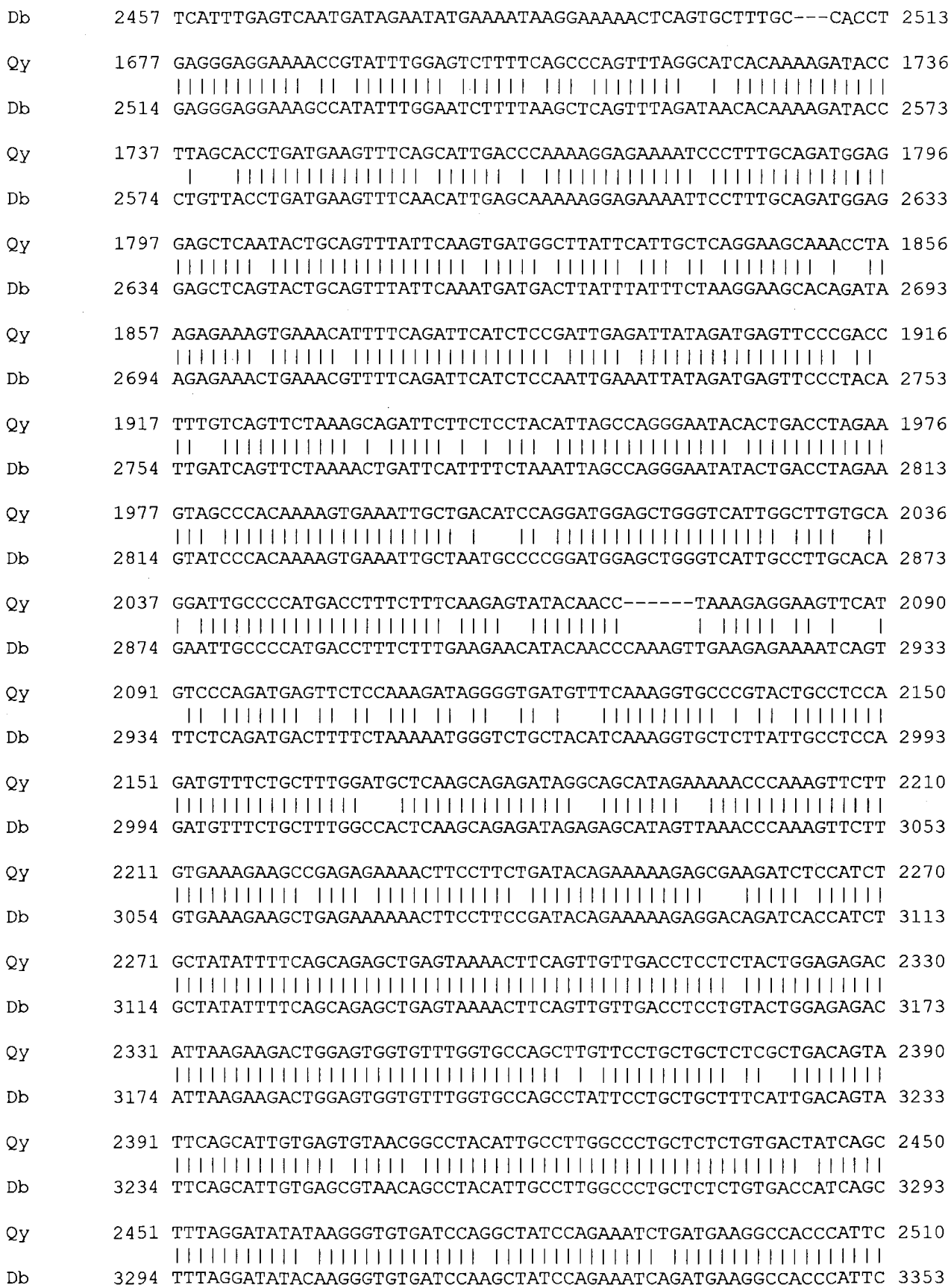

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Qy       2571 TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT 2630
             |||||||||||||||| |||||||| ||||| |||||||| ||||||||||||||||||
Db       3414 TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT 3473

Qy       2631 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 2690
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Db       3474 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 3533

Qy       2691 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT 2750
             ||||| |||||||||||||||| |||||||||| ||||||||||||||||||||||||
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Qy       2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
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Db       3654 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3713

Qy       2871 GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT 2930
               || |||  ||| | |||       ||||||| ||||||||||||||||||||||||||
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Qy       2931 CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC------ 2984
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Db       3769 ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG 3827

Qy       2985 -----AGATCTTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG 3038
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Qy       3039 CCCTGTGTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT 3098
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Qy       3099 ATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATT 3158
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RESULT 4
US-10-717-597-310
; Sequence 310, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.

; APPLICANT: Twine, Natalie C.
; APPLICANT: Dorner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 310
; LENGTH: 4053
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-310

Query Match 62.1%; Score 2379.4; DB 17; Length 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

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Qy        181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
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Qy        241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
              |||||||||| |||||| | |||| | || |||| |||||||| | |||||||||  |
Db       1086 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1145

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Db       1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205

Qy        361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
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Qy        421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
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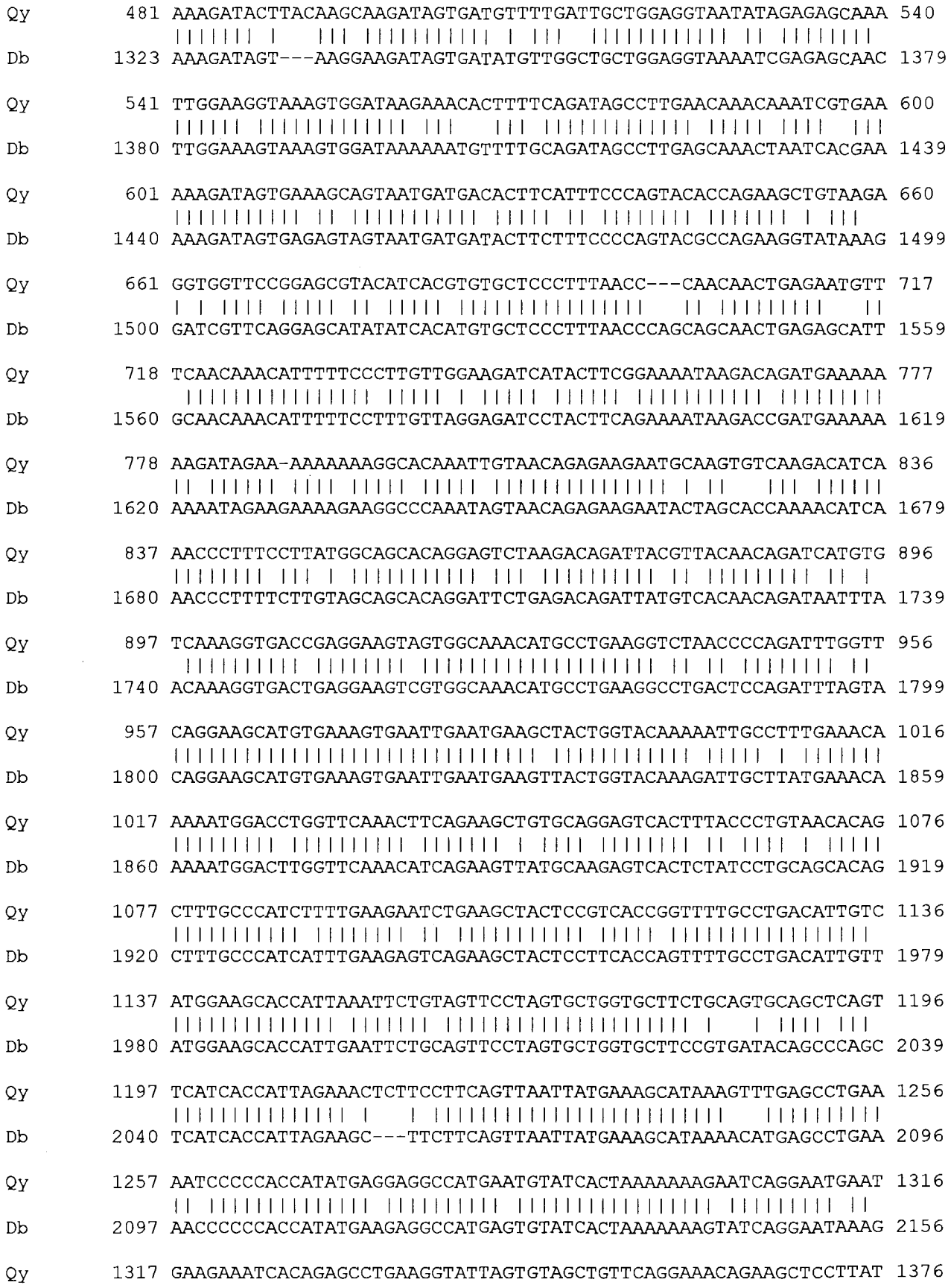

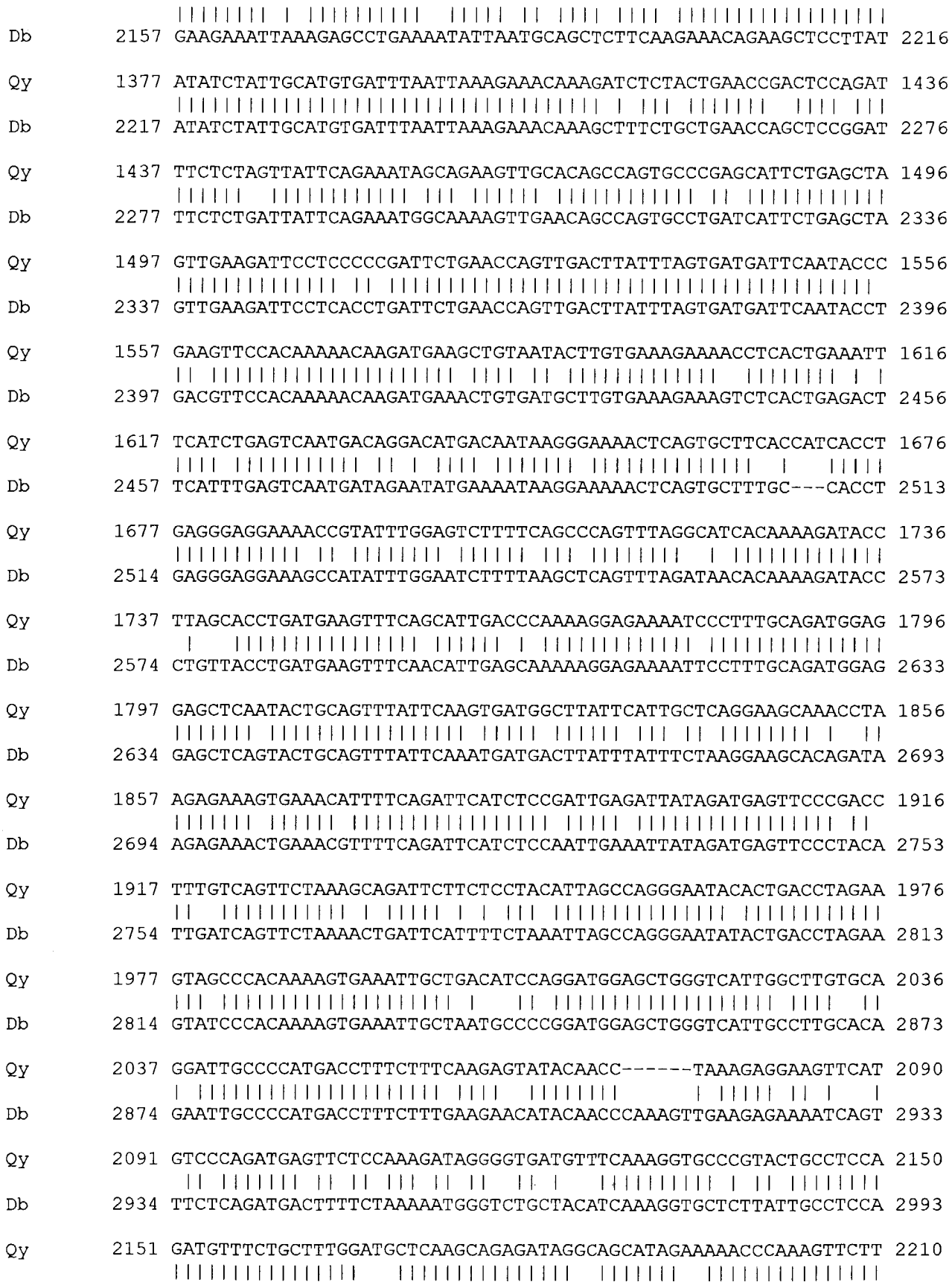

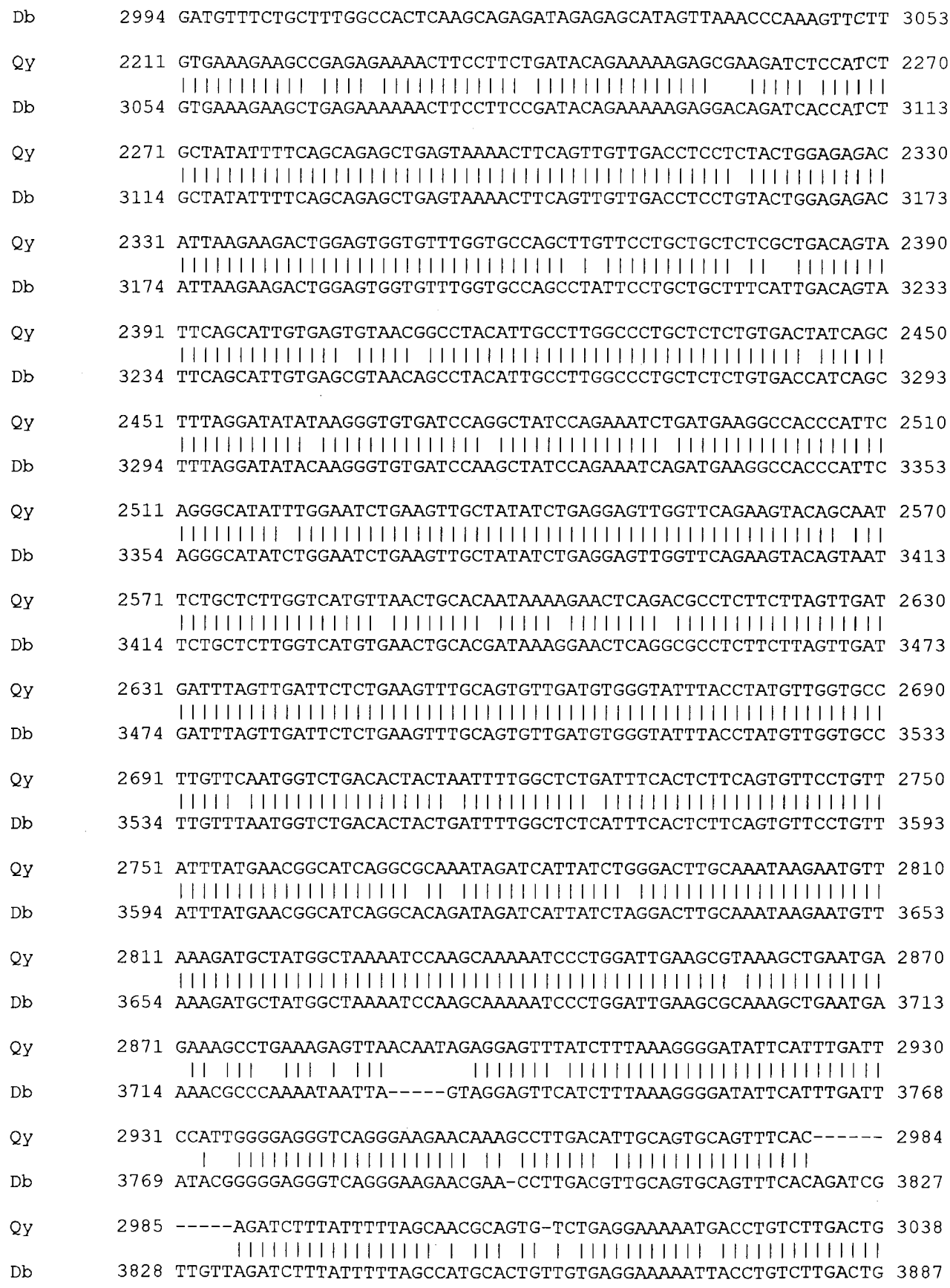

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RESULT 5
US-09-789-386-1
; Sequence 1, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-789-386-1

Query Match 58.0%; Score 2223.6; DB 9; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
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Db        772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
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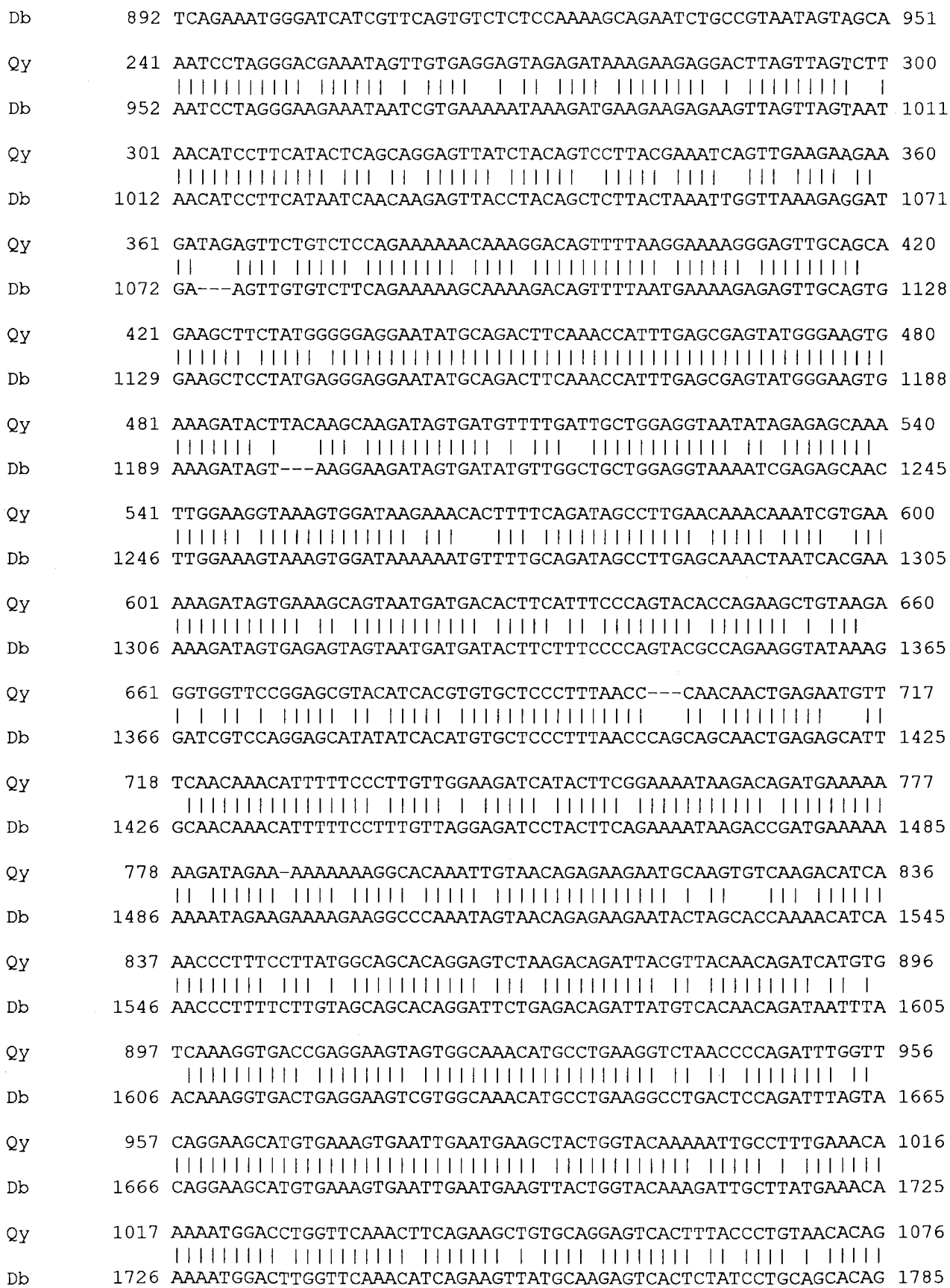

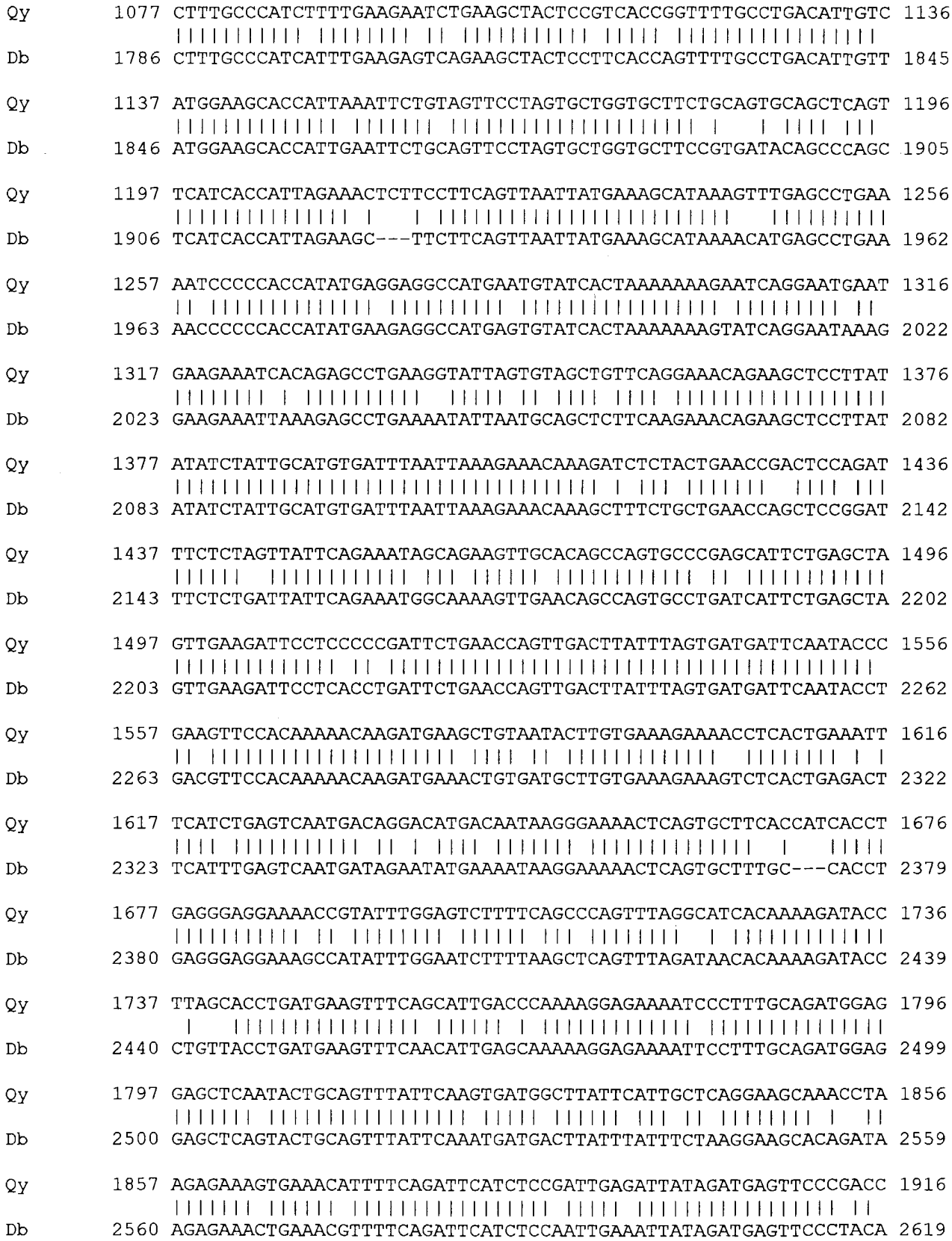

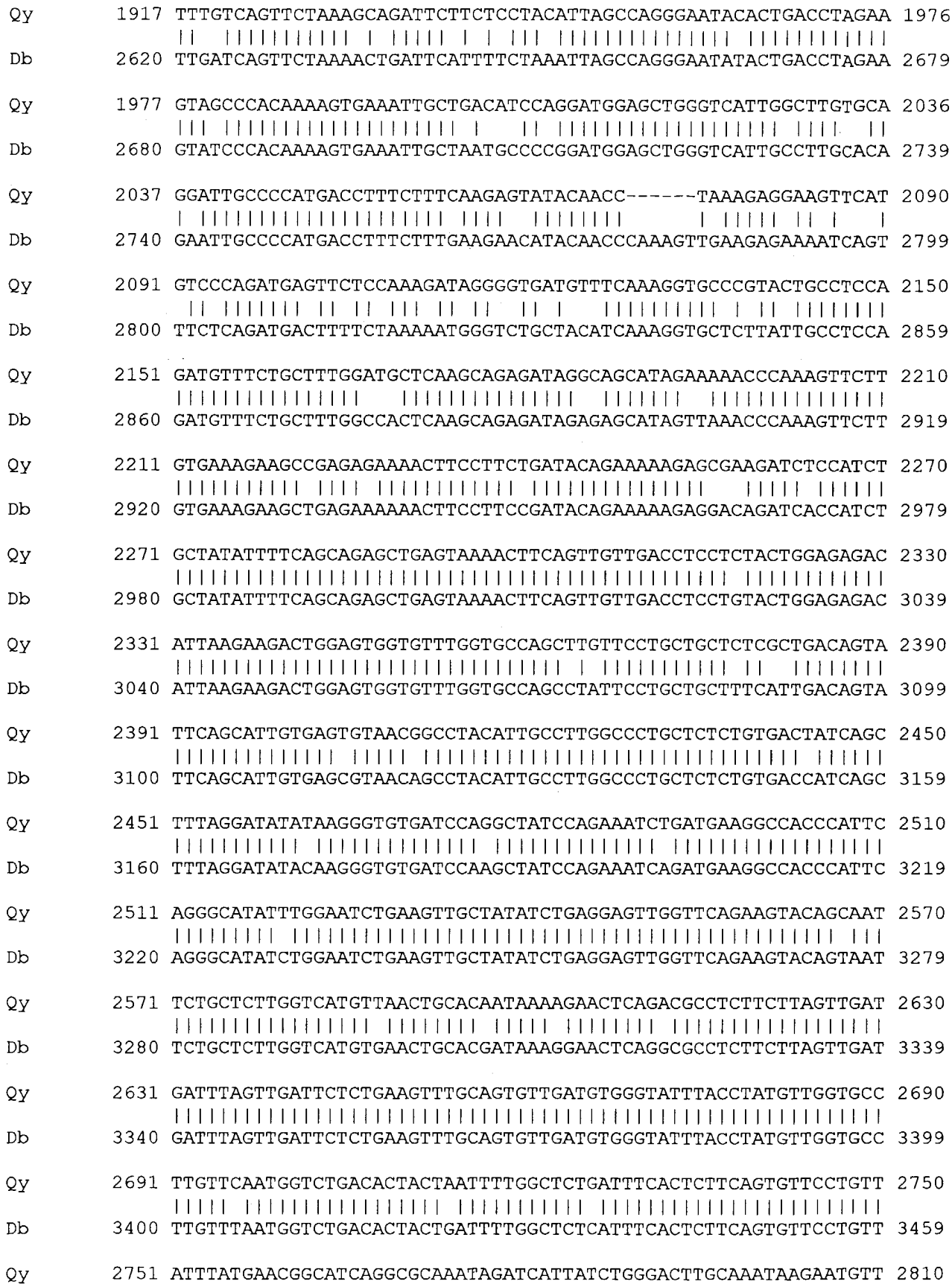

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RESULT 6
US-09-893-348-22
; Sequence 22, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
;  APPLICANT: EISENBACH-SCHWARTZ, Michal
;  APPLICANT:  COHEN, Irun R.
;  APPLICANT:  BESERMAN, Pierre
;  APPLICANT:  MOSONEGO, Alon
;  APPLICANT:  MOALEM, Gila
;  TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
;  FILE REFERENCE: EIS-SCHWARTZ=2A
;  CURRENT APPLICATION NUMBER: US/09/893,348
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/314,161
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: US 09/218,277
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: PCT/US98/14715
;  PRIOR FILING DATE: 1998-07-21
;  PRIOR APPLICATION NUMBER: IL 124500
;  PRIOR FILING DATE: 1998-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
;   LENGTH: 3579
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3579)
;   OTHER INFORMATION:
US-09-893-348-22

  Query Match             58.0%;  Score 2223.6;  DB 9;  Length 3579;
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  Matches 2519;  Conservative    0;  Mismatches  339;  Indels   22;  Gaps    7;

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Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
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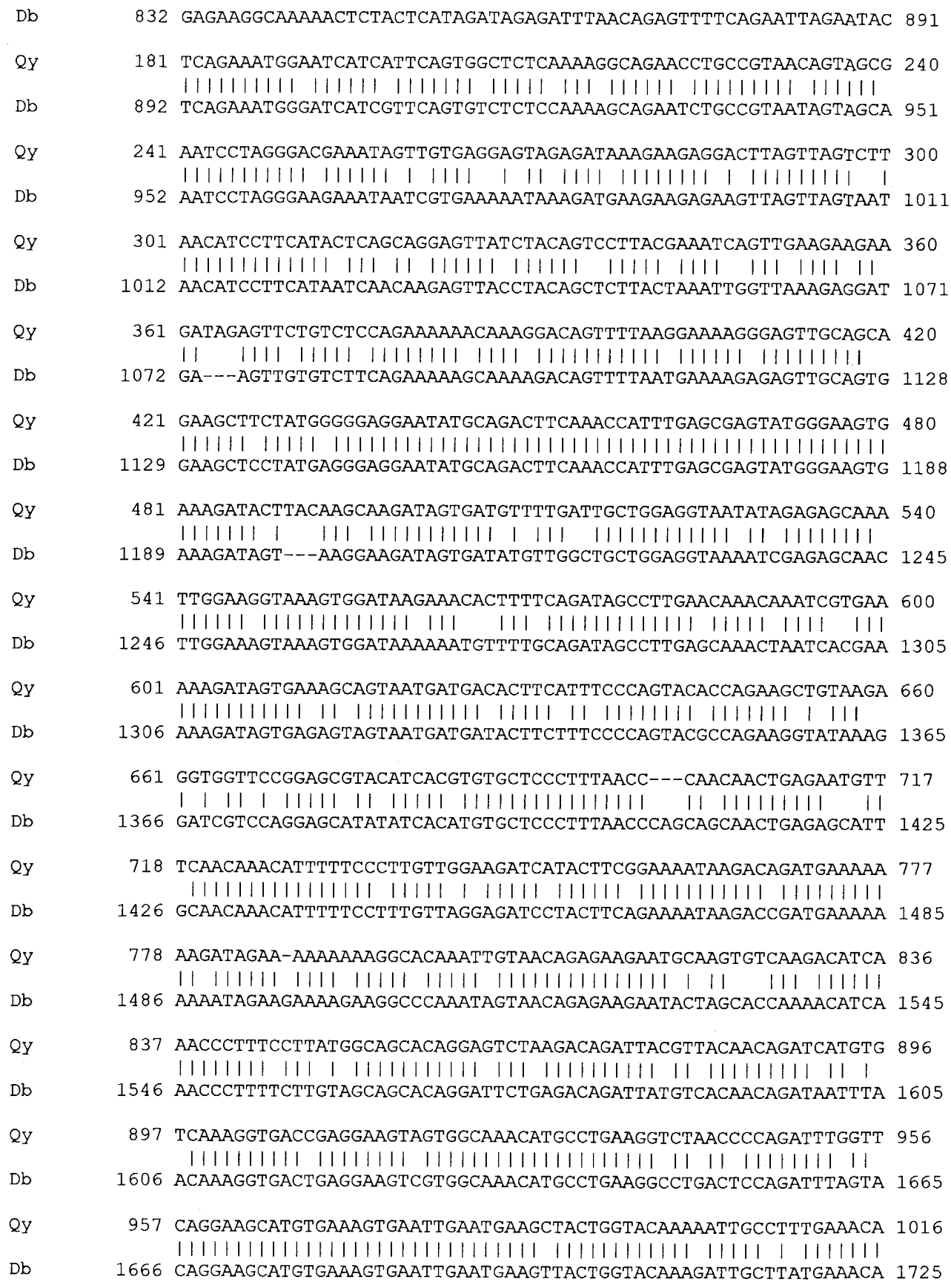

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Qy       1557 GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT 1616
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Db       2263 GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT 2322

Qy       1617 TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT 1676
             |||| |||||||||||| || | |||| ||||||| |||||||||||||  |   |||||
Db       2323 TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGC---CACCT 2379

Qy       1677 GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC 1736
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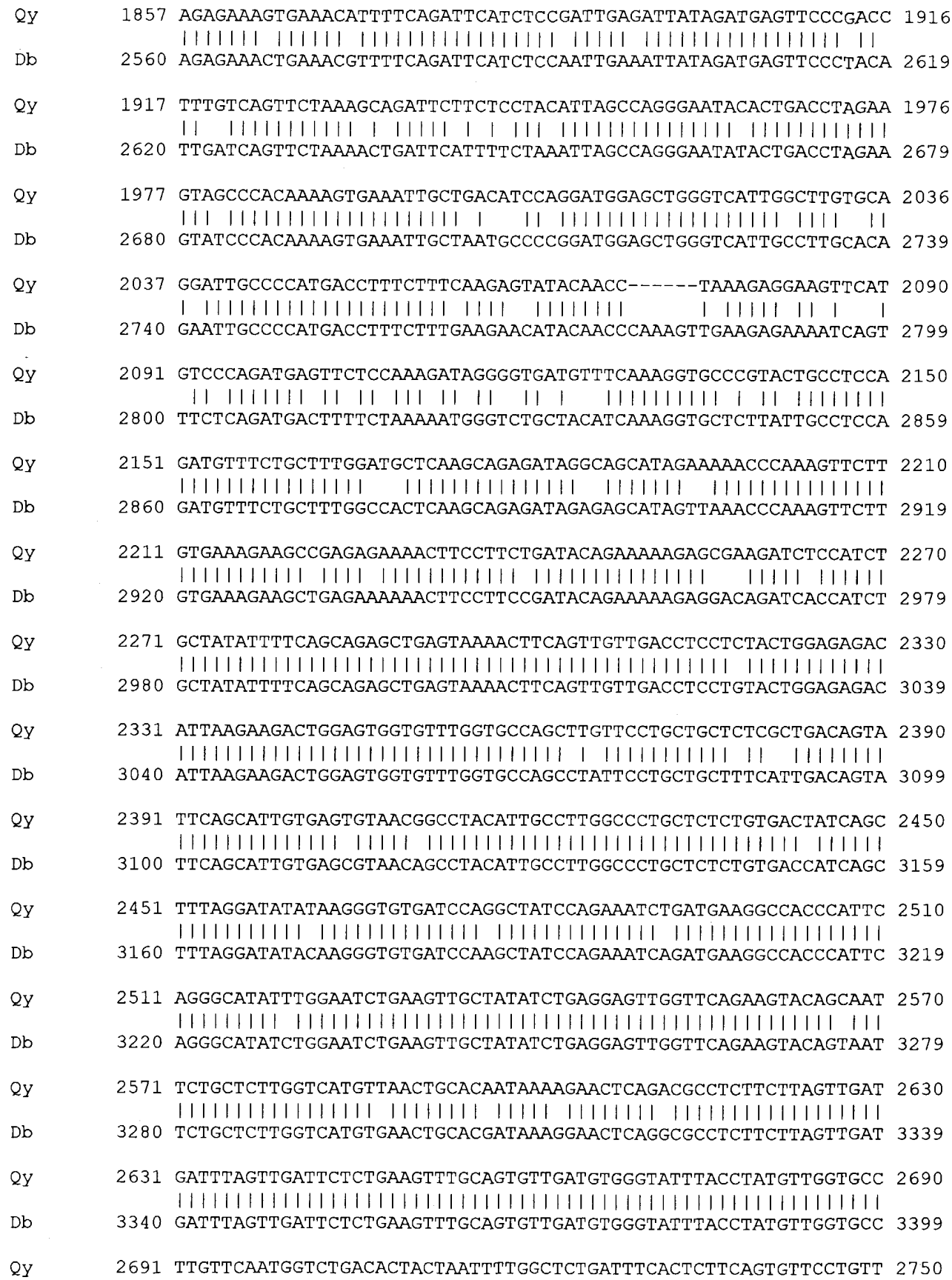

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RESULT 7
US-10-267-502-212
; Sequence 212, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
;  APPLICANT: Kim, Jaeseob
;  APPLICANT:  Galant, Ron
;  TITLE OF INVENTION: Obesity Linked Genes
;  FILE REFERENCE: LSD-07416
;  CURRENT APPLICATION NUMBER: US/10/267,502
;  CURRENT FILING DATE:  2003-01-27
;  NUMBER OF SEQ ID NOS: 439
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 212
;   LENGTH: 3579
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-267-502-212

  Query Match             58.0%;  Score 2223.6;  DB 12;  Length 3579;
  Best Local Similarity   87.5%;  Pred. No. 0;
  Matches 2519;  Conservative    0;  Mismatches  339;  Indels   22;  Gaps    7;

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Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
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Qy        241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
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Db        952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy        301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
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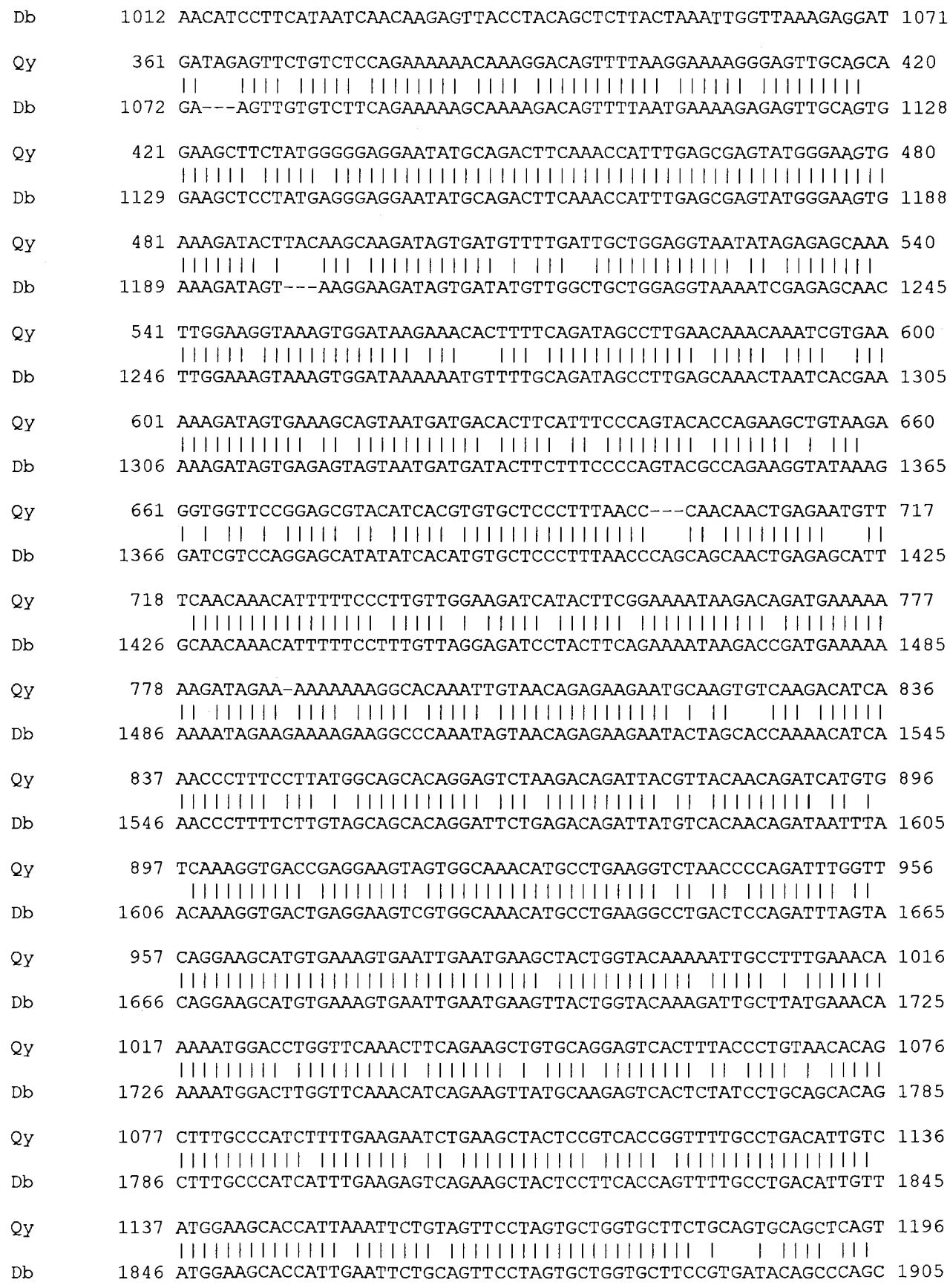

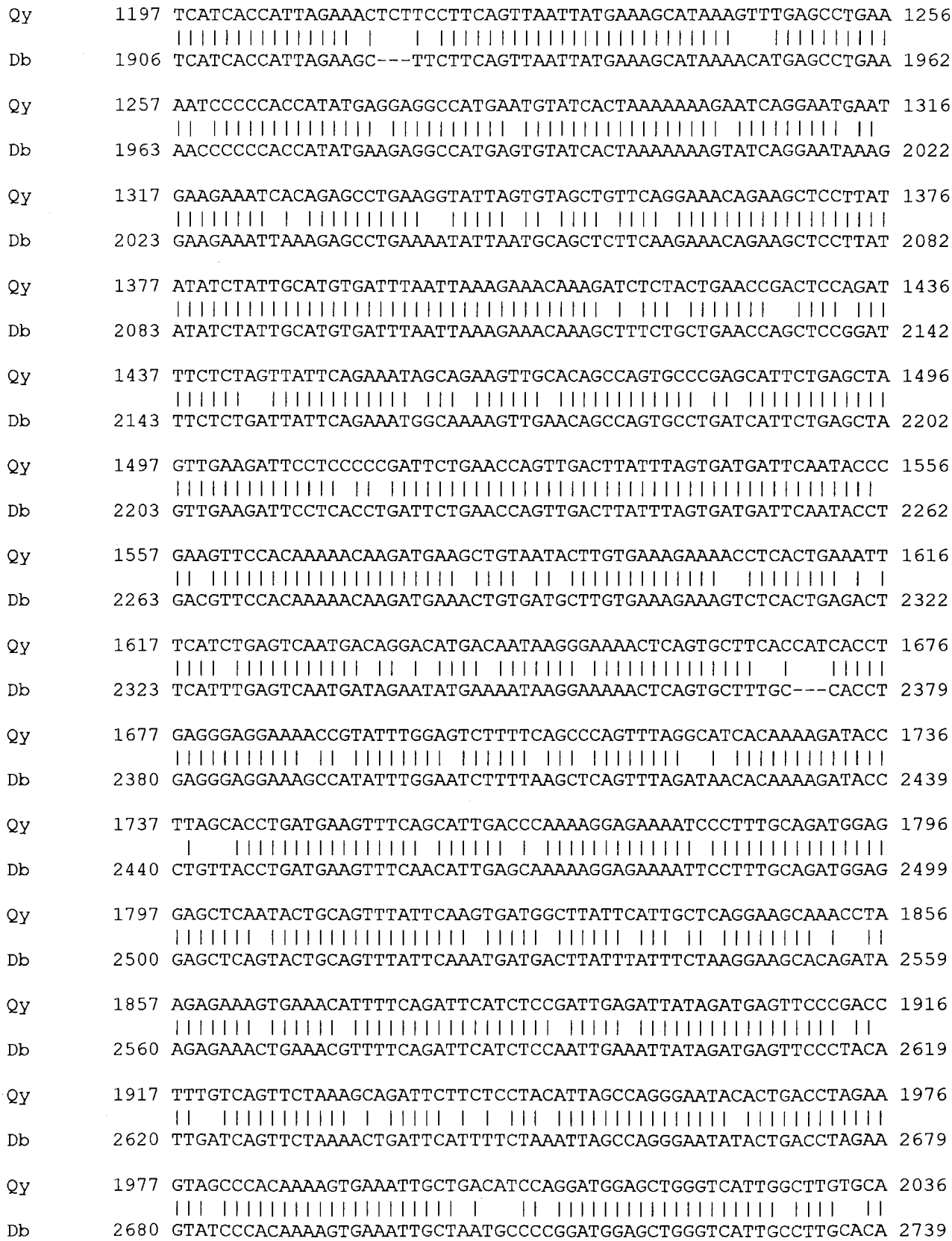

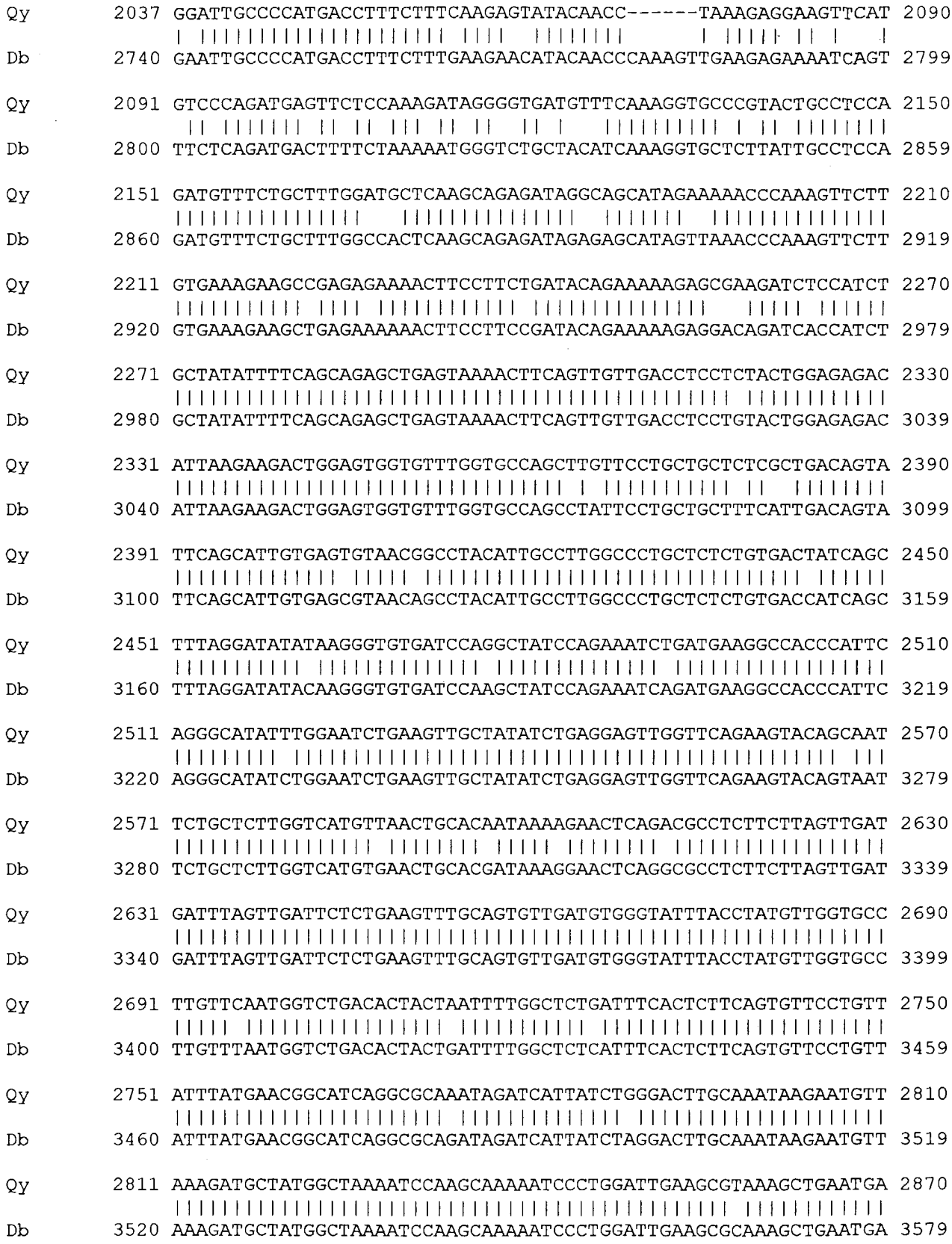

RESULT 8
US-10-327-213-8
; Sequence 8, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
; APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-327-213-8

Query Match 58.0%; Score 2223.6; DB 17; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy        301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
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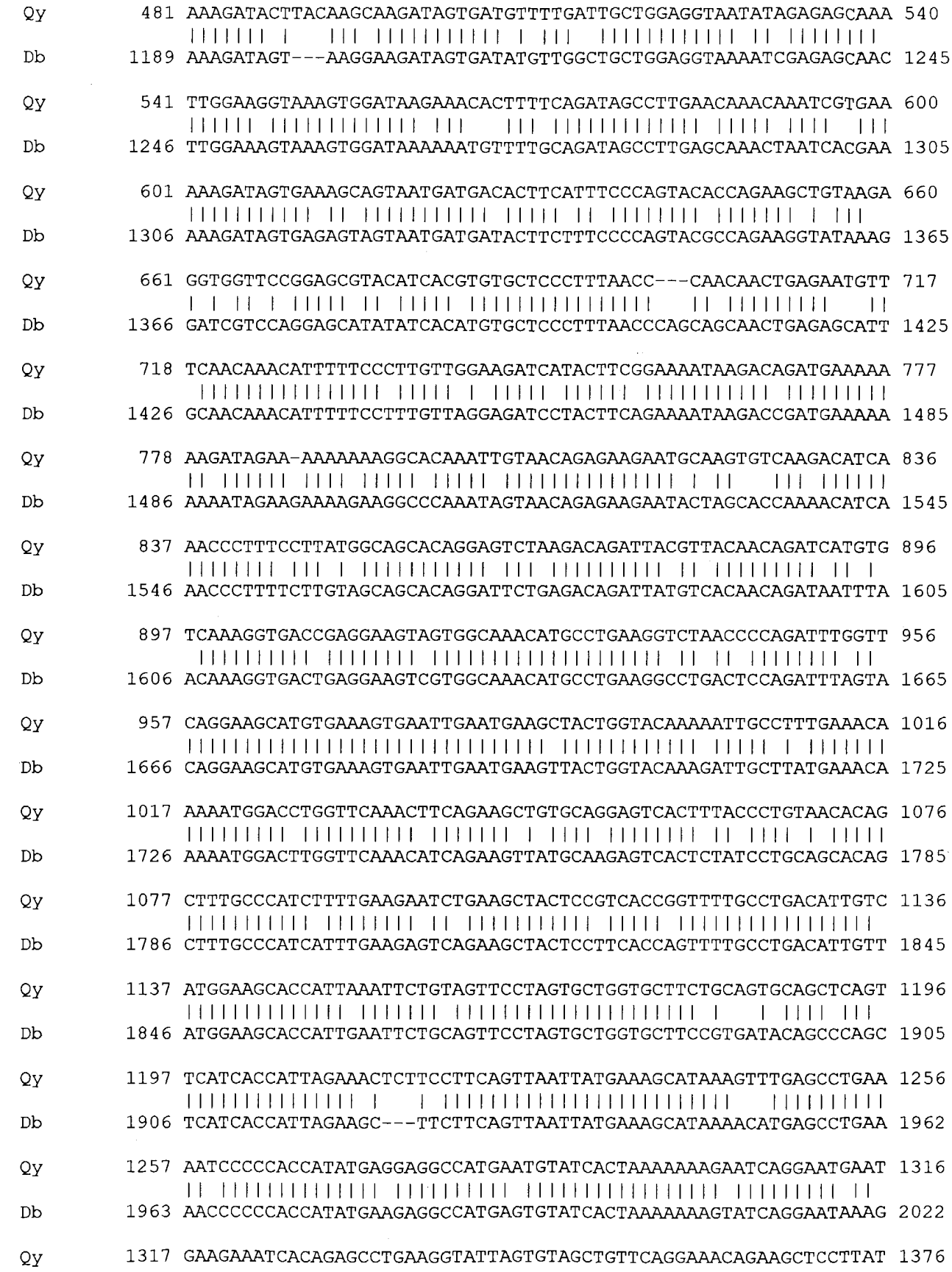

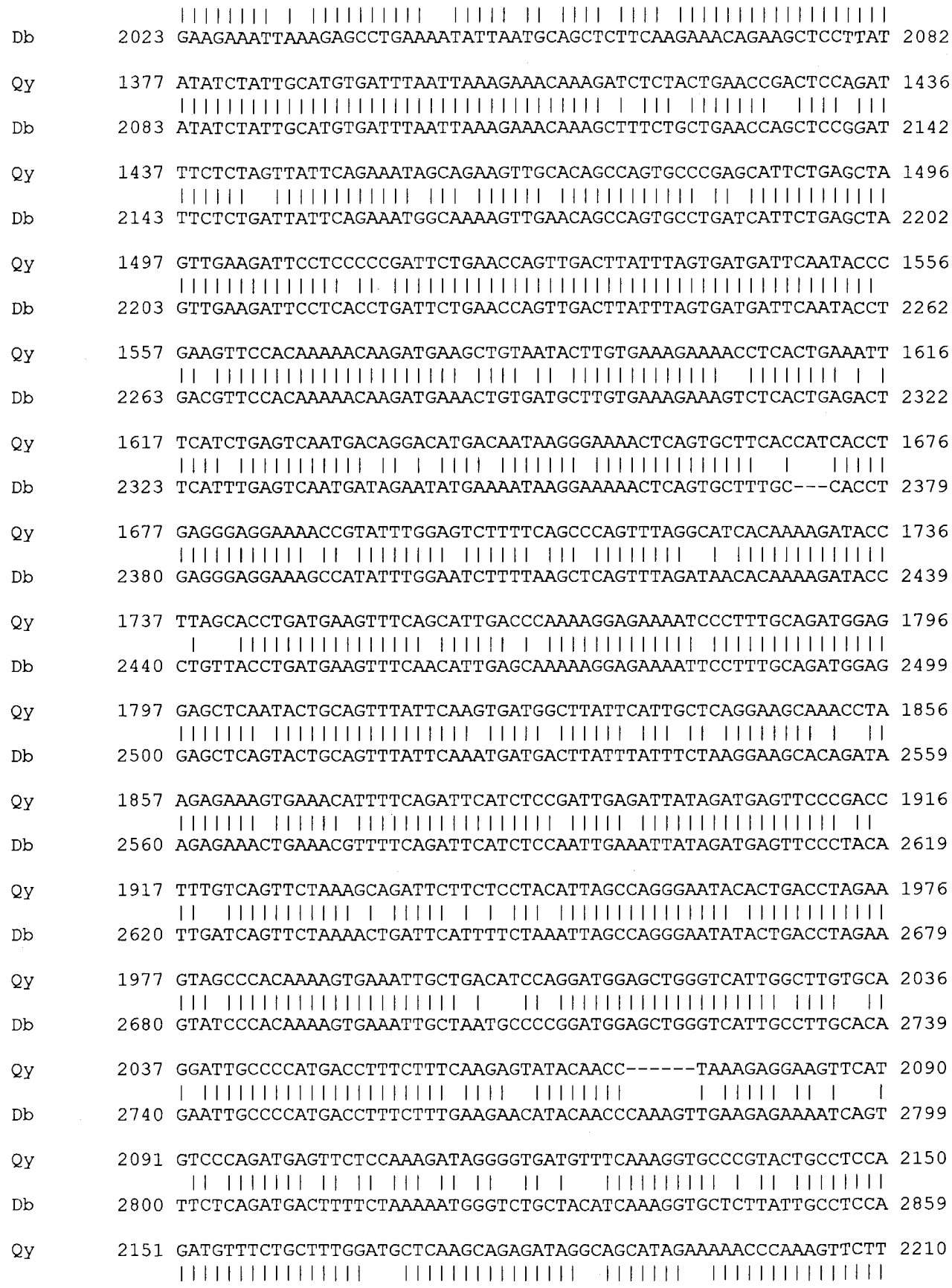

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Qy       2331 ATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTA 2390
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Qy       2391 TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC 2450
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Db       3100 TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC 3159

Qy       2451 TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC 2510
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RESULT 9
US-10-466-258-8
; Sequence 8, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15

; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
US-10-466-258-8

Query Match 58.0%; Score 2223.6; DB 17; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
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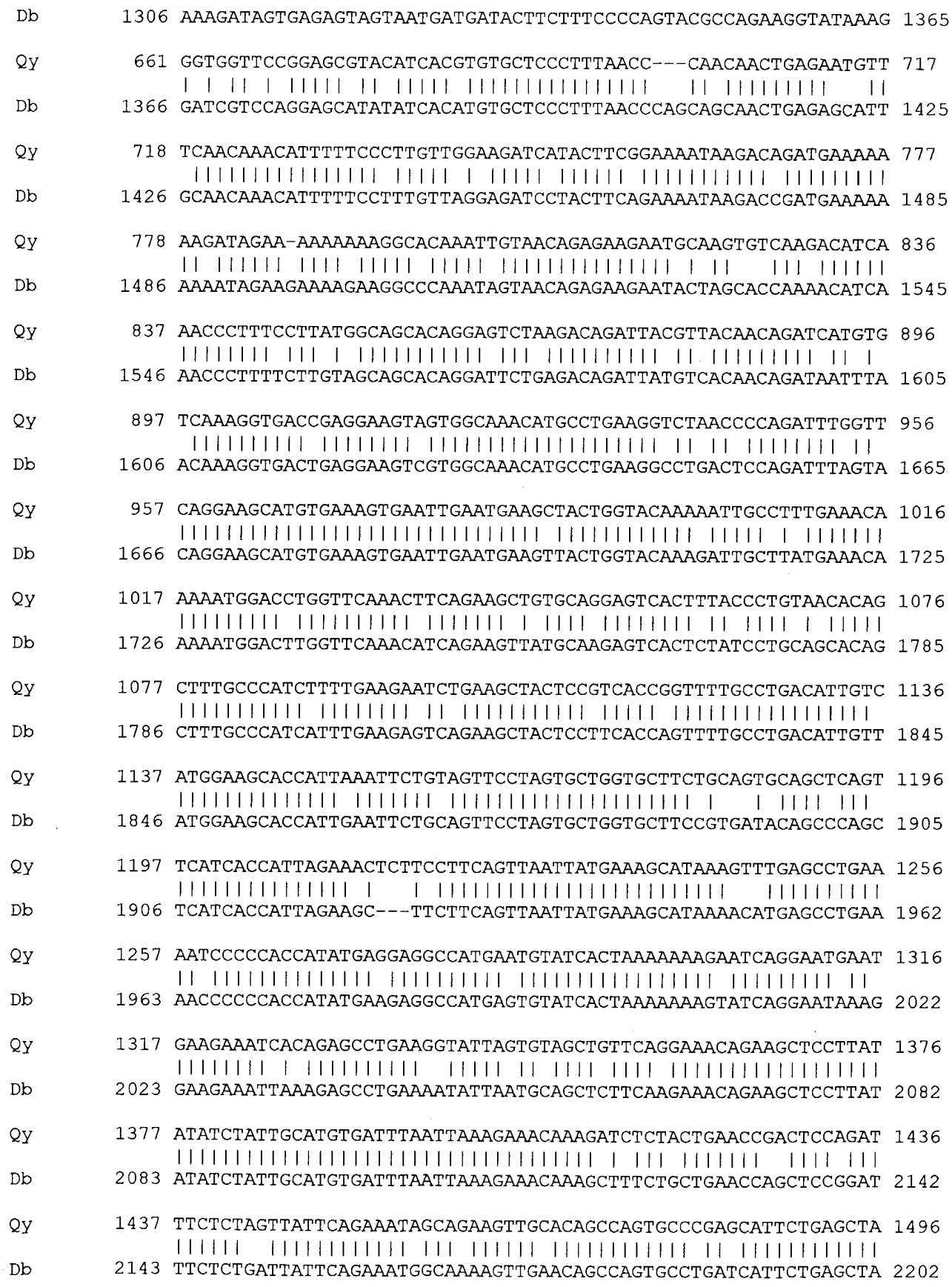

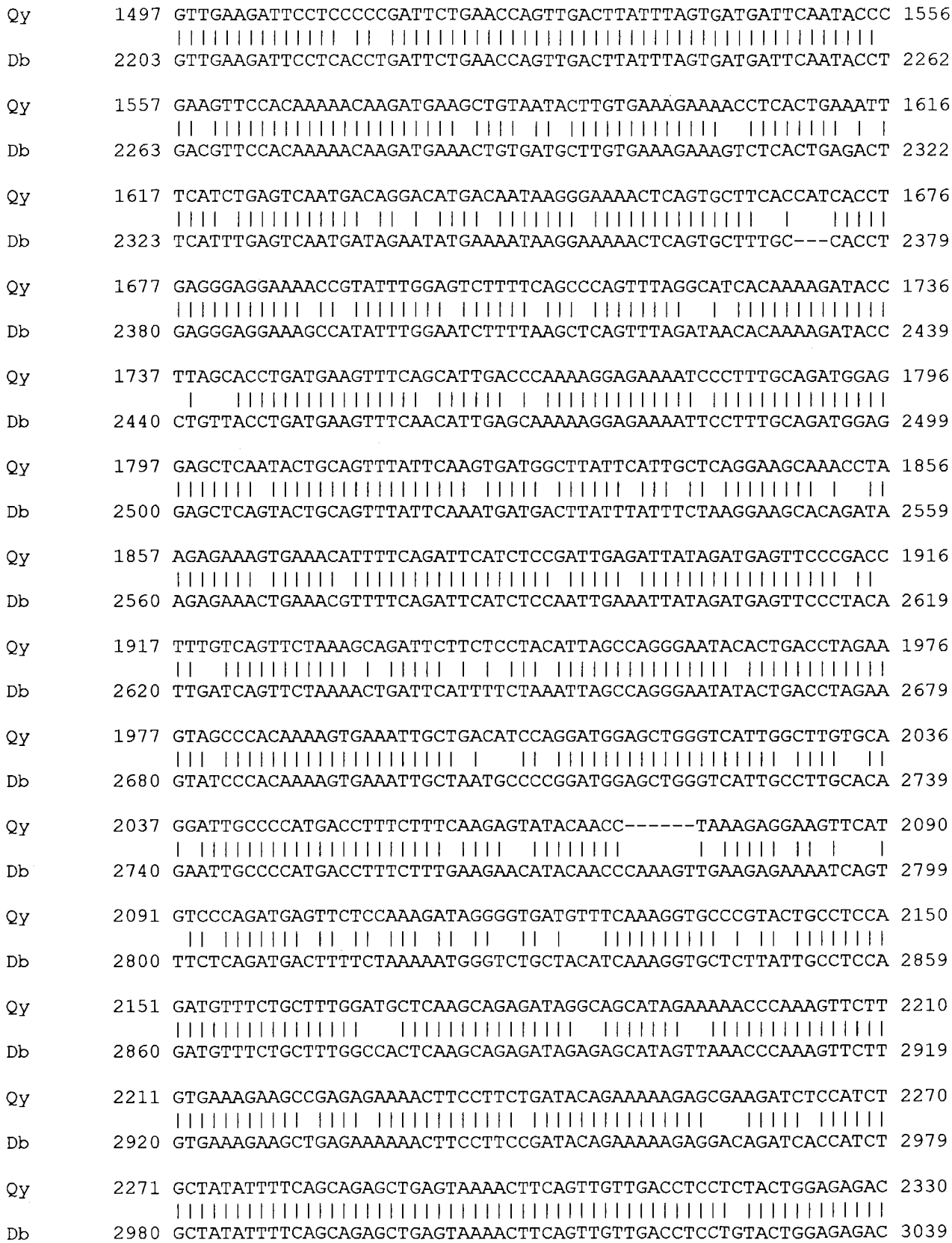

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RESULT 10
US-09-893-348-17
; Sequence 17, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
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;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (253)..(3744)
;   OTHER INFORMATION:
US-09-893-348-17

Query Match 56.9%; Score 2179.4; DB 9; Length 4684;
Best Local Similarity 78.2%; Pred. No. 0;
Matches 3008; Conservative 0; Mismatches 731; Indels 110; Gaps 28;

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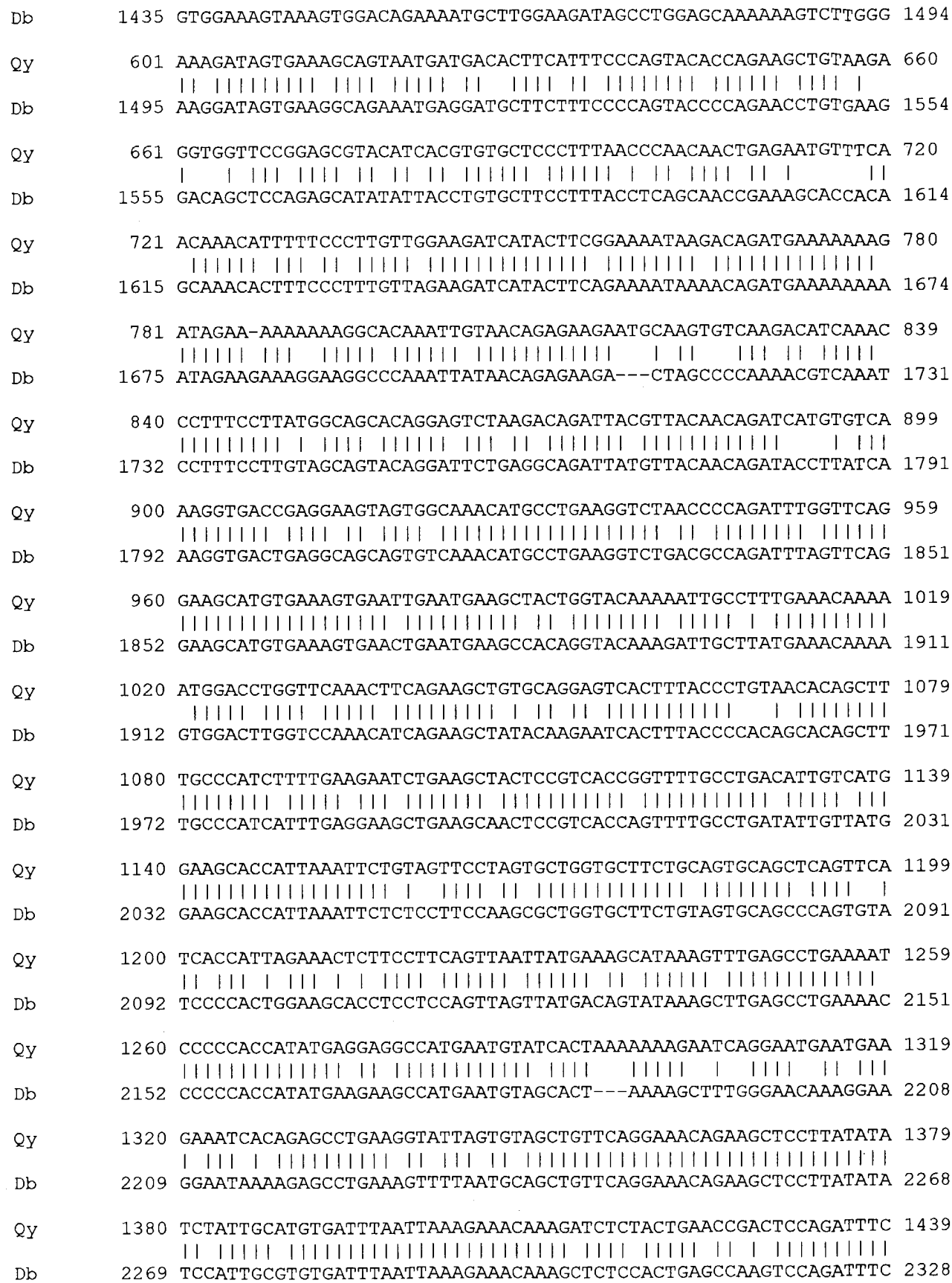

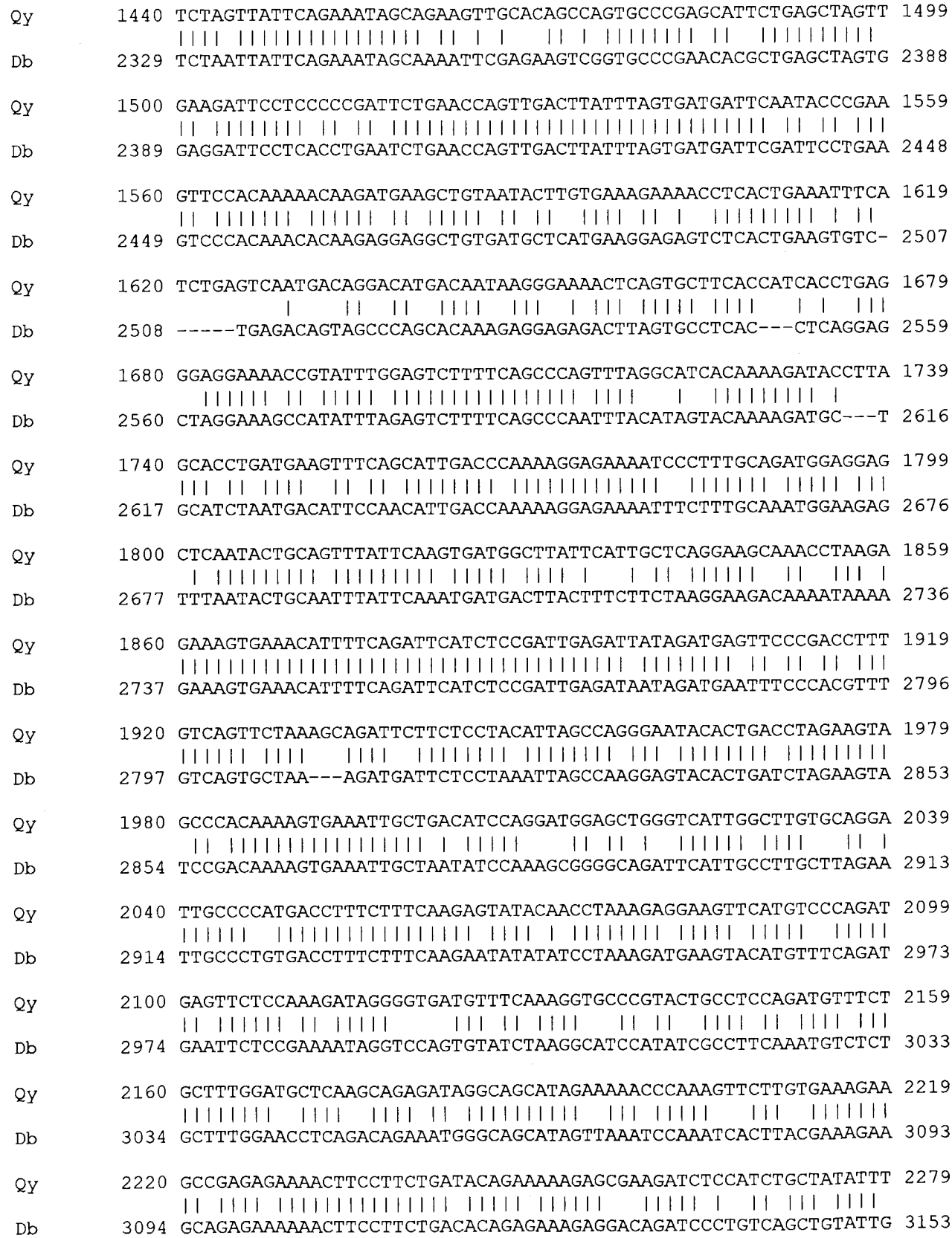
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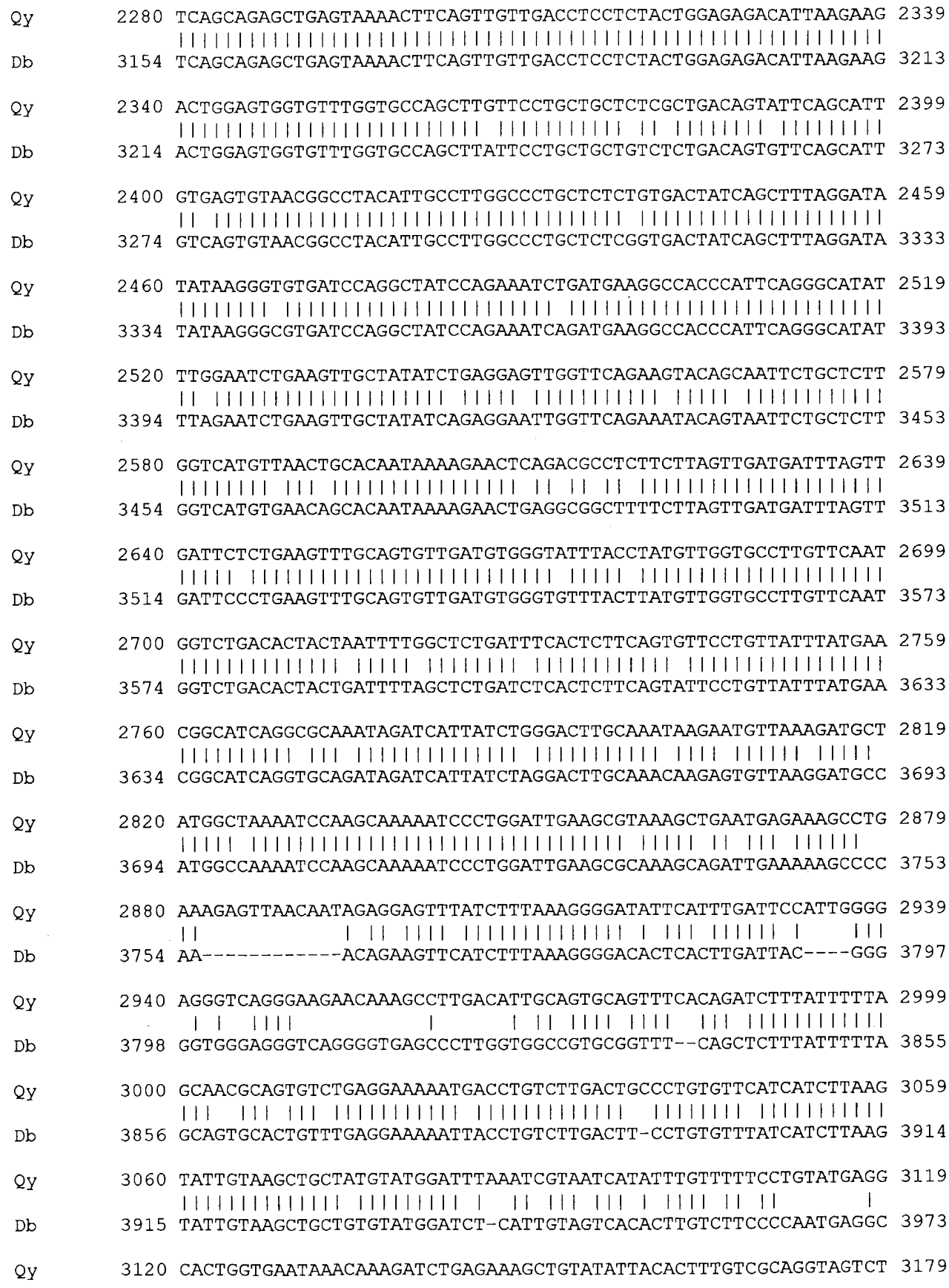
Qy 1500 GAAGATTCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAA 1559
Db 2389 GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAA 2448
Qy 1560 GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA 1619
Db 2449 GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC- 2507
Qy 1620 TCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAG 1679
Db 2508 -----TGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCAC---CTCAGGAG 2559
Qy 1680 GGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTA 1739
Db 2560 CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---T 2616
Qy 1740 GCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAGGAG 1799
Db 2617 GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAG 2676
Qy 1800 CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGA 1859
Db 2677 TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA 2736
Qy 1860 GAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT 1919
Db 2737 GAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTT 2796
Qy 1920 GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA 1979
Db 2797 GTCAGTGCTAA---AGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA 2853
Qy 1980 GCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCAGGA 2039
Db 2854 TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAA 2913
Qy 2040 TTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCCAGAT 2099
Db 2914 TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGAT 2973
Qy 2100 GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCT 2159
Db 2974 GAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCT 3033
Qy 2160 GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA 2219
Db 3034 GCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAA 3093
Qy 2220 GCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT 2279
Db 3094 GCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTATTG 3153



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Db       3974 GCCTGGTGAATAAAGGA--CTCGGGGAAAGCTGTGCATTGTATCTGCTGCAGGGTAGTCT 4031

Qy       3180 TGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCT---GACAGAAATAACCCTTTTCACA 3236
                ||||||||   | || ||| ||||||  |   | ||   | |||  | ||||||||||||
Db       4032 AGCTGTATGCAGAGAGTTGTAAAGAAGGCAAATCTGGGGGCAGGGAAAACCCTTTTCACA 4091

Qy       3237 GTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTA 3296
                |  |||  |  |||  |      |||  |  |         ||||||||||||||||||||
Db       4092 G--TGTACTGTGTTTGGTCAGTGTAAAACTGATGCAGATTTTTCTGAAATGAAATGTTTA 4149

Qy       3297 GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGG 3356
                || ||||  |||  |  ||  ||  ||||    |||||  ||  |  ||  ||||  |||||||||
Db       4150 GATGAGAGCATACTACTAAAGCAGAGTGGAAAACTCTGTC--TTTATGGTGTGTTCTAGG 4207

Qy       3357 TGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATA 3416
                |||||||||  ||||||||||  |||    ||||||||||||||||||||||        |
Db       4208 TGTATTGTG-AATTTACTGTTATAT----TGCCAATATAAGTAAATATAGA----CCTAA 4258

Qy       3417 TCTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTT 3476
                ||||||||||||||||||  ||||||||  |||||  |  |  ||||||||||||||||||
Db       4259 TCTATATATAGTGTTTCACAAAGCTTAGATCTTTAACCTTGCAGCTGCCCCACAGTGCTT 4318

Qy       3477 GATACTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACG 3536
                ||    |  |||||  ||||  |    |||||||||  |   ||  |  |       ||||||  |
Db       4319 GACCTCTGAGTCATTGGTTAT-GCAGTGTAGTCCAAGCACATAAACTAGGAAGAGAAATG 4377

Qy       3537 TACTTCTAGGCGCACTACC-ATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACT 3595
                ||  ||  ||||  |  |||||  |  |    |  |    ||  |||    |     |   |  ||||  ||  |
Db       4378 TATTTGTAGGAGTGCTACCTACCACCTGTTTTCAAGAAAATATAGAACTCCAACAAAAAT 4437

Qy       3596 CCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTC----- 3650
                    ||   |  |   |   |   |   |   |   | ||||||||||| |||||  ||||
Db       4438 ATAGAATGTCATTTCAAAGACTTACTGTATGTATAGTTAATTTTGTCACAGACTCTGAAA 4497

Qy       3651 -----TGGACTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTA 3705
                     ||||||||||  |  ||||||||  ||||||||||  |||||||||||||||||  |
Db       4498 TTCTATGGACTGAATTTCATGCTTCC--AAATGTTTGCAGTTATCAAACATTGTTATGCA 4555

Qy       3706 AGAAAATAT-AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGT 3764
                |||||  ||  ||||||  ||  ||||||  ||||||||||||||  |||  ||||  |  ||||||
Db       4556 AGAAATCATAAAATGAAGACTTATACCATTGTGGTTTAAGCCGTACTGAATT--ATCTGT 4613

Qy       3765 GGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAA 3824
                ||||||||||||||||||||||||||||||||||||||||||||||||||  | ||||||||
Db       4614 GGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGATCTTAAAAAAAA 4673

Qy       3825 AAAAAAAAA 3833
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Db       4674 AAAAAAAAA 4682
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RESULT 11
US-10-267-502-214
; Sequence 214, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:

; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214
; LENGTH: 3492
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-267-502-214

Query Match 48.7%; Score 1866; DB 12; Length 3492;
Best Local Similarity 80.9%; Pred. No. 0;
Matches 2325; Conservative 0; Mismatches 500; Indels 49; Gaps 11;

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Qy          1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
              |||||||||||||||| | | | ||||||||||||  | ||||||||||| | ||| |||||
Db        664 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACACGGATACCTTGGTAACTTATCAGCA 723

Qy         61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
              ||     |||| |||||||| ||  || ||||| |||||||||||||| || |||  ||
Db        724 GTGGCATCCACAGAAGGAACTATTGAAGAAACTTTAAATGAAGCTTCTAGAGAATTGCCA 783

Qy        121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
              |||| ||||| |||||||||||||| | ||| | | | |||| ||||||| ||| |||||
Db        784 GAGAGGGCAACAAATCCATTTGTAAATAGAGAGTCAGCAGAGTTTTCAGTATTAGAATAC 843

Qy        181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
              |||||||||| |||||| |||| |||||| | ||| | |||  | ||| |   |||||
Db        844 TCAGAAATGGGATCATCTTTCAATGGCTCCCCAAAAGGAGAGTCAGCCATGTTAGTAGAA 903

Qy        241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
              ||  ||| ||| ||| || |||||||||||| ||| |   ||||||| |||||| ||  |
Db        904 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACA---AAGAGGATTTAGTTTGTAGT 960

Qy        301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
                   |||||||| ||  || |||| | || |   |||||| |||   ||| |||||||
Db        961 GCAGCCCTTCATAATCCACAAGAGTCACCTGCGACCCTTACTAAAGTGGTTAAAGAAGAC 1020

Qy        361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
              |   ||||| |||||||||||||| |||| ||||| |||||| |||| |  | |  |||
Db       1021 G---GAGTTATGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGAAAATGTCAGTG 1077

Qy        421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
              | |||  || || |||| || |||||||| || || |||||||| | || ||||||||||
Db       1078 GTAGCACCTGTGAGGGAAGAGTATGCAGATTTTAAGCCATTTGAACAAGCATGGGAAGTG 1137

Qy        481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
              ||||||||||  ||  |  ||| |||||  ||  |||| ||| |||||
Db       1138 AAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATA---------- 1186

Qy        541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
               ||||| |||||||||| || |||  ||||  ||||||||| || |||| || || ||
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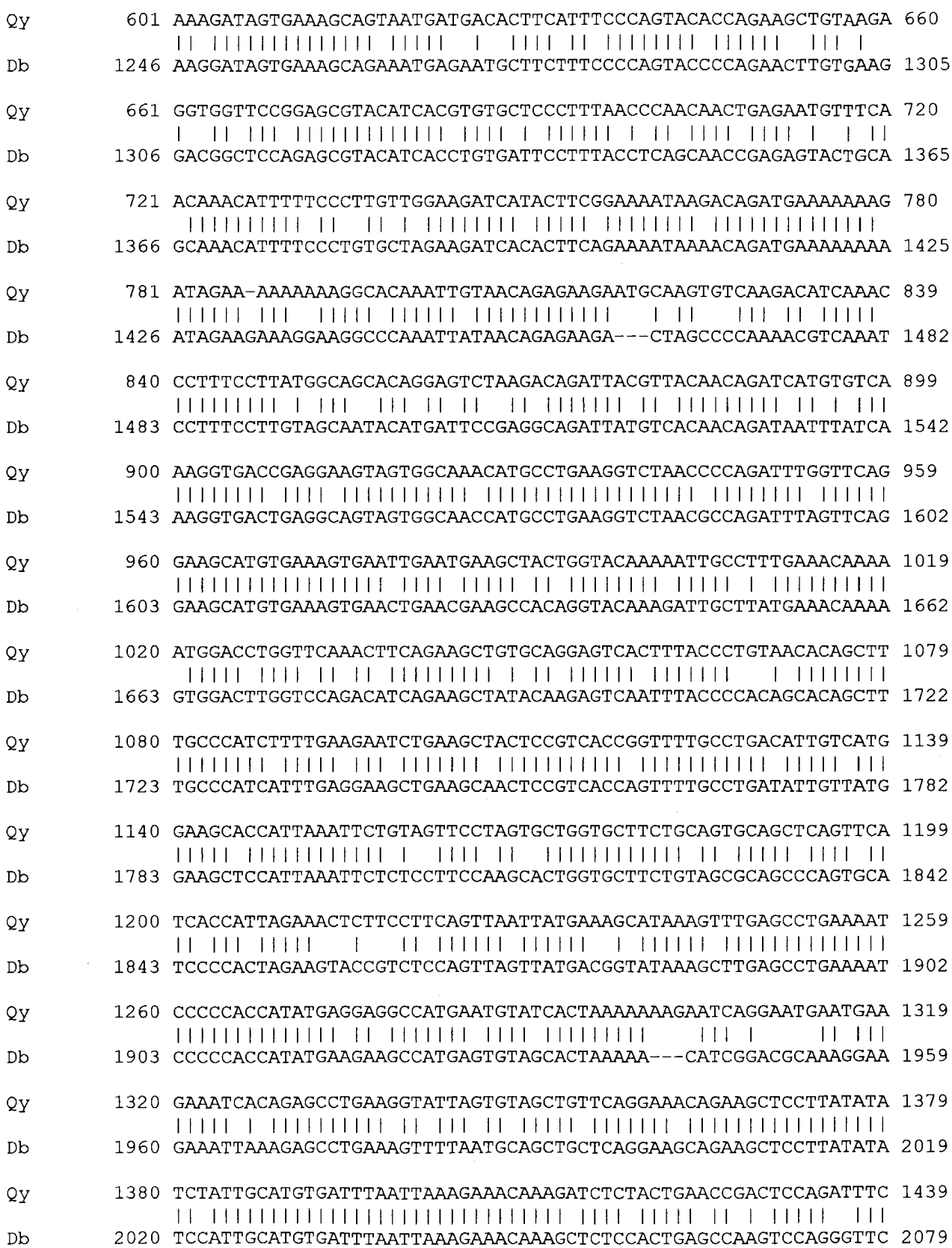

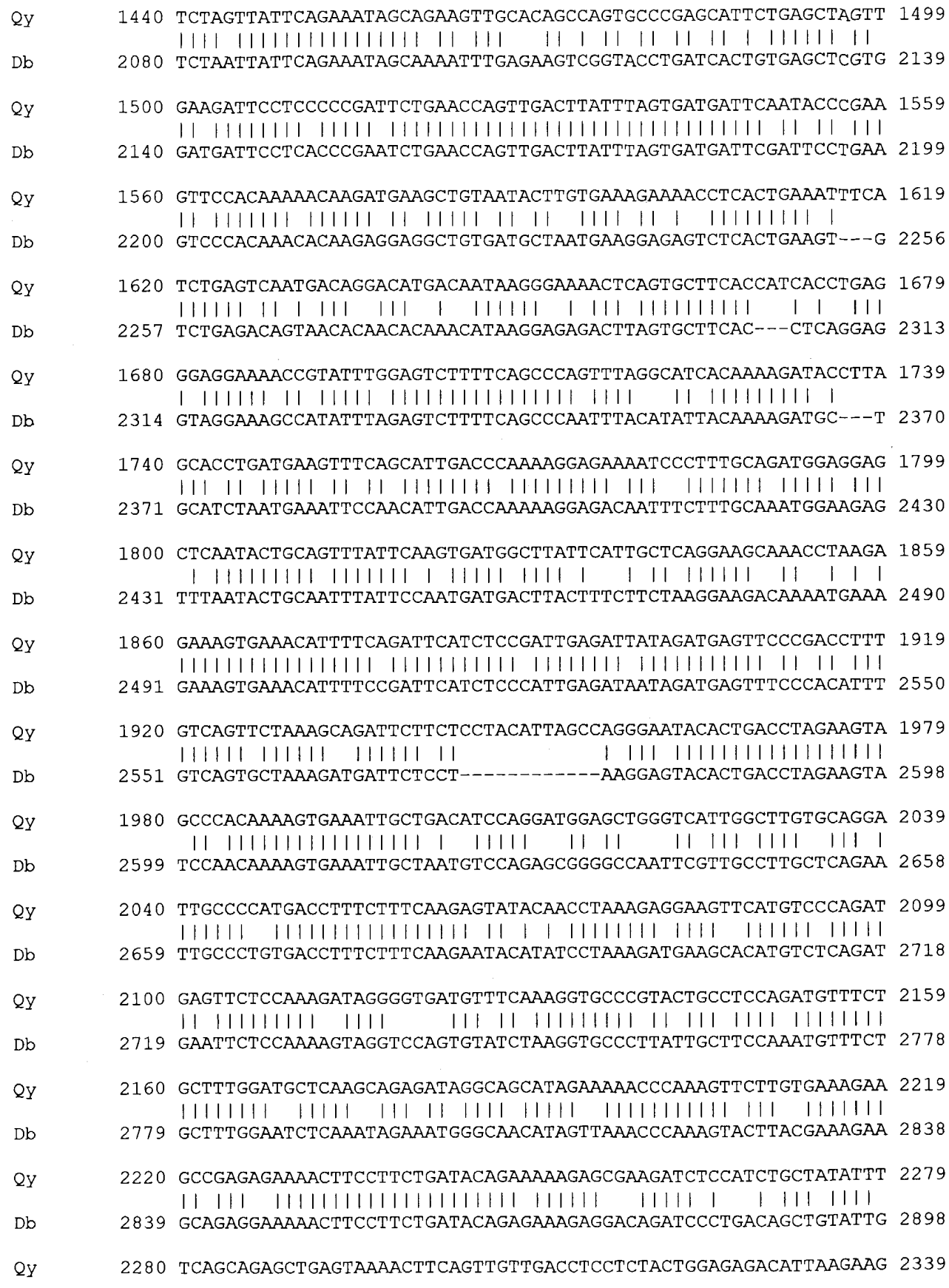

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Db       2899 TCAGCAGAGCTGAATAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAG 2958

Qy       2340 ACTGGAGTGGTG---TTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTATTCAGC 2396
                ||||||||||||   |||||||||||||| |||||||||| || |||||||| ||||||
Db       2959 ACTGGAGTGGTGTATTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC 3018

Qy       2397 ATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGG 2456
                ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3019 ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGG 3078

Qy       2457 ATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCA 2516
                |||||||||||||||||||| |||||||||||||| ||||||||||||||||||||||||
Db       3079 ATATATAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3138

Qy       2517 TATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCT 2576
                |||||||||||||||||||| ||||| ||||| |||||||||| || || |||||||||
Db       3139 TATTTGGAATCTGAAGTTGCCATATCAGAGGAATTGGTTCAGAAATATAGTAATTCTGCT 3198

Qy       2577 CTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTA 2636
                |||||||||||  ||| |||||||||||||  | || || ||||||||||||||||||||
Db       3199 CTTGGTCATGTGAACAGCACAATAAAAGAATTGAGGCGTCTCTTCTTAGTTGATGATTTA 3258

Qy       2637 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTC 2696
                ||||||||  |||||||||||||||||||||||||||||||| || ||||||||||||||
Db       3259 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTATTTACTTACGTTGGTGCCTTGTTC 3318

Qy       2697 AATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTAT 2756
                ||||||  |||||||||  |||||  ||||||||  |||||||||||  |||||||||| |||
Db       3319 AATGGTTTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATATAT 3378

Qy       2757 GAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGAT 2816
                ||||||||||||||||  |||||||||||||  ||||||||||  ||||  |||||  |||
Db       3379 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGCGTTAAGGAT 3438

Qy       2817 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
                ||  |||||  |||||||||||||||||||||||||||||||  |||||  ||||||
Db       3439 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGAATGA 3492
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RESULT 12
US-10-220-891-22
; Sequence 22, Application US/10220891
; Publication No. US20030207286A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERITICS OF ENHANCED
; TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE
PROGNOSIS
; TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH
FAVORABLE
; TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE
PROGNOSIS
; FILE REFERENCE: 7388-73435
; CURRENT APPLICATION NUMBER: US/10/220,891
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: JP 2000/140387

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: JP 2000/159195
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
;   LENGTH: 1980
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-220-891-22

  Query Match   36.9%; Score 1414.6; DB 16; Length 1980;
  Best Local Similarity   87.0%; Pred. No. 0;
  Matches 1671; Conservative   0; Mismatches 209; Indels   41; Gaps   9;

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Qy       1326 ACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTATATATCTATT 1385
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Db         28 AAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATT 87

Qy       1386 GCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCTCTAGT 1445
              ||||||||||||||||||||||||||| | ||| ||||||| |||| |||||||||  |
Db         88 GCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGAT 147

Qy       1446 TATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTTGAAGAT 1505
              |||||||||||  ||| |||||| |||||||||||  || ||||||||||||||||||||
Db        148 TATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTTGAAGAT 207

Qy       1506 TCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAGTTCCA 1565
              |||||  || ||||||||||||||||||||||||||||||||||||||||  || ||||||
Db        208 TCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCA 267

Qy       1566 CAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCATCTGAG 1625
              |||||||||| |||| |||| || ||||||||||||  |||||||| | ||||| ||||
Db        268 CAAAAACAAGGTGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGAG 327

Qy       1626 TCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAGGGAGGA 1685
              ||||||| || | |||| ||||||| |||||||||||||  |   ||||||||||||||
Db        328 TCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGC---CACCTGAGGGAGGA 384

Qy       1686 AAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAGCACCT 1745
              || || |||||||| |||||| ||| ||||||||  | |||||||||||||  |   ||||
Db        385 AAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCT 444

Qy       1746 GATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAGGAGCTCAAT 1805
              |||||||||||| |||||| | |||||||||||||  |||||||||||||||||||||  |
Db        445 GATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGT 504

Qy       1806 ACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGAGAAAGT 1865
              ||||||||||||||||  ||||| |||||| ||| || |||||||| |  ||||||||  |
Db        505 ACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACT 564

Qy       1866 GAAACATTTTCAGATTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTTGTCAGT 1925
              |||||  |||||||||||||||||  |||||  ||||||||||||||||||  ||  |||||
Db        565 GAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGT 624

Qy       1926 TCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTAGCCCAC 1985
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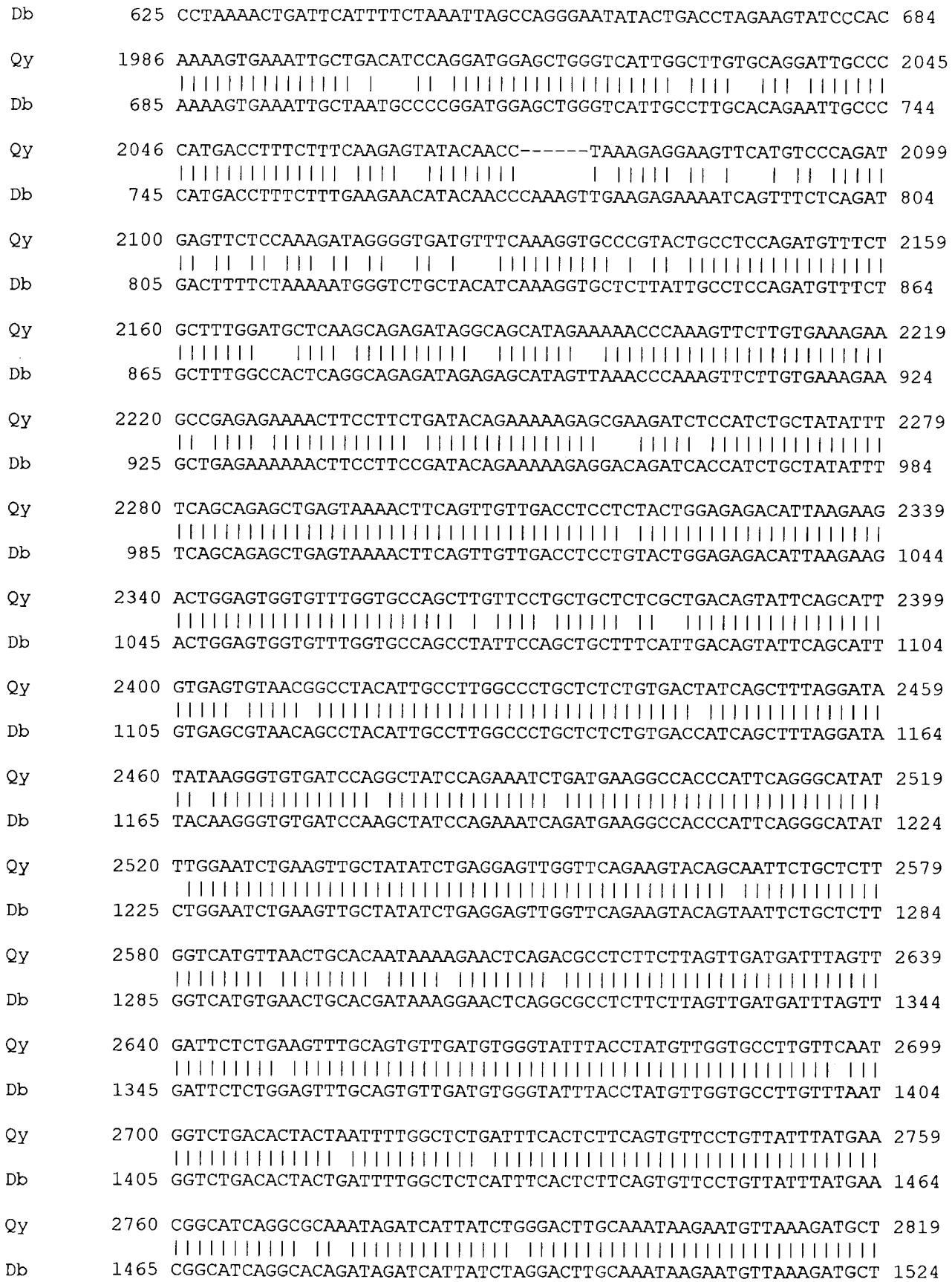

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Qy       2820 ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTG 2879
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Db       1525 ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCA 1584

Qy       2880 AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGG 2939
             ||| | |||       ||||||| ||||||||||||||||||||||||||  | ||||
Db       1585 AAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATTATACGGGGG 1639

Qy       2940 AGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC----------AGAT 2988
             ||||||||||||||| || ||||||| |||||||||||||||||          ||||
Db       1640 AGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGAT 1698

Qy       2989 CTTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTT 3047
             |||||||||||| | ||| || | |||||||||| |||||||||||||| ||||||
Db       1699 CTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTT 1758

Qy       3048 CATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTT- 3106
             |||||||||||||||||||||||||||||||| |||||| |||||||||| | |||
Db       1759 CATCATCTTAAGTATTGTAAGCTGCTATGTATGGGTTTAAACCGTAATCATATCTTTTTC 1818

Qy       3107 -TTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTT 3165
              |  || | ||||||||||||| |           | | ||| |||||||||  |||||
Db       1819 CTATCTATCTGAGGCACTGGTGGA----------ATAAAAAACCTGTATATTTTACTTT 1867

Qy       3166 GTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATA 3224
             || |||| ||||||||| | || |||| | ||||| ||| |||||||| | ||| |
Db       1868 GTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAA 1927

Qy       3225 A 3225
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Db       1928 A 1928
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RESULT 13
US-10-060-036-54
; Sequence 54, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
;  APPLICANT: Benson, Darin R.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Persing, David H.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Jiang, Yuqiu
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF PANCREATIC CANCER
;  FILE REFERENCE: 210121.566
;  CURRENT APPLICATION NUMBER: US/10/060,036
;  CURRENT FILING DATE:  2002-01-30
;  NUMBER OF SEQ ID NOS: 4560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
;   LENGTH: 2235
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-036-54
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Query Match 26.8%; Score 1025.4; DB 15; Length 2235;
Best Local Similarity 86.7%; Pred. No. 5.2e-249;
Matches 1361; Conservative 0; Mismatches 131; Indels 77; Gaps 18;

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Qy       2304 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 2363
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Db        697 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 756

Qy       2364 TTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
              | |||||||||||  ||  ||||||||||||||||||||||  |||||  ||||||||||||
Db        757 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 816

Qy       2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
             ||||||||||||||||||||  ||||||||||||||||  ||||||||||||||  ||||||
Db        817 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 876

Qy       2484 CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
             ||||||||  ||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        877 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 936

Qy       2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAA 2603
             ||||||||||||||||||||||  ||||||||||||||||||  ||||||||  |||||
Db        937 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 996

Qy       2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 2663
             ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        997 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 1056

Qy       2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT 2723
             ||||||||||||||||||||||||||||||  ||||||||||||||||  |||||||||
Db       1057 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 1116

Qy       2724 CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
             ||  ||||||||||||||||||||||||||||||||||||||||||||  ||  |||||||||
Db       1117 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1176

Qy       2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
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Db       1177 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1236

Qy       2844 CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT 2903
             |||||||||||||| |||||||||||  ||  |||  |||  |  |||        |||||||
Db       1237 CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTC 1291

Qy       2904 ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTT 2963
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Db       1292 ATCTTTAAAGGGGATATTCATTTGATTATACGGGGGAGGGTCAGGGAAGAACGAA-CCTT 1350

Qy       2964 GACATTGCAGTGCAGTTTCAC----------AGATCTTTATTTTTAGCAACGCAGTG-T 3011
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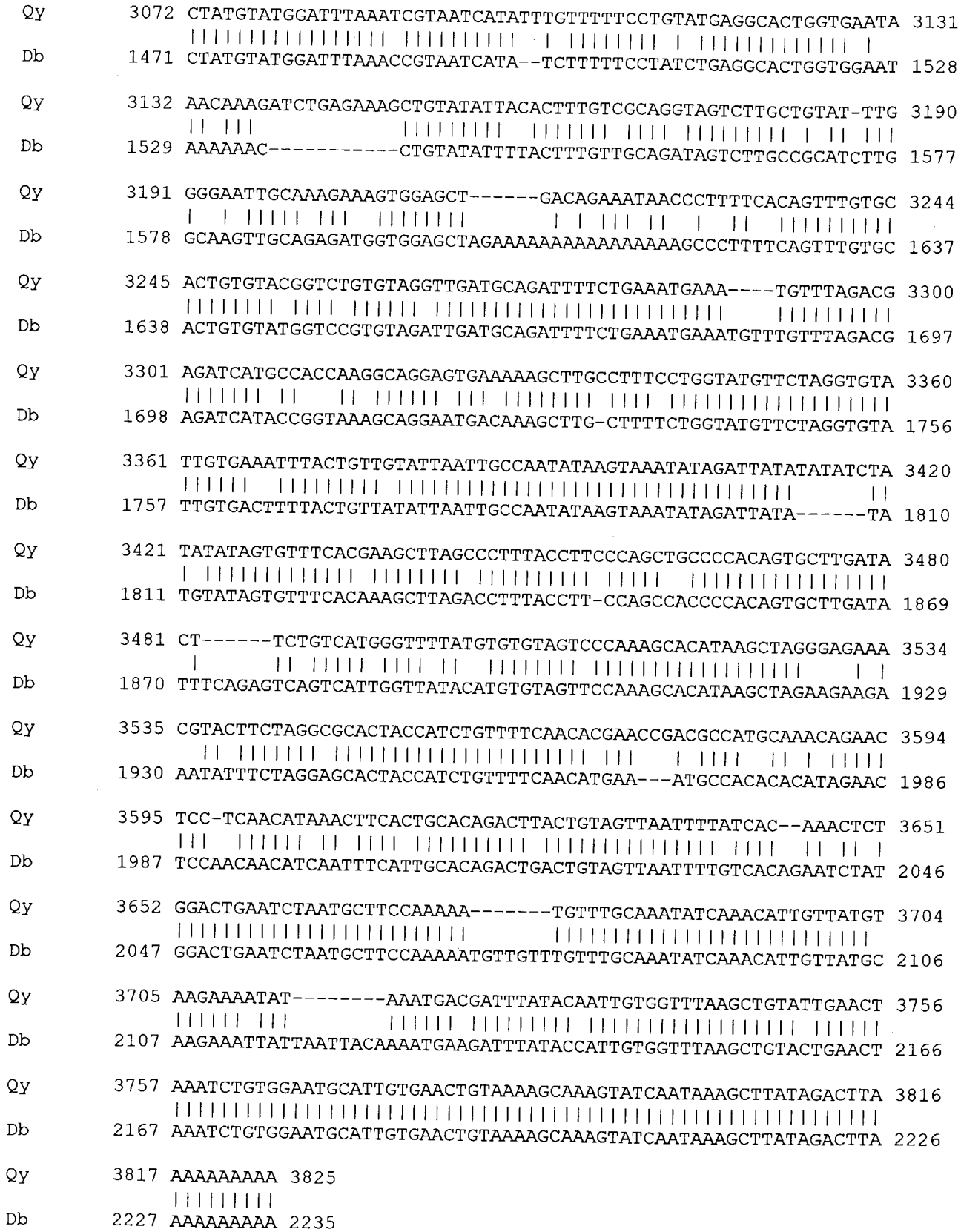

RESULT 14
US-09-823-245A-349
; Sequence 349, Application US/09823245A
; Publication No. US20020039760A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6401
; CURRENT APPLICATION NUMBER: US/09/823,245A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/194,941
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 349
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-245A-349

Query Match 25.8%; Score 989.2; DB 13; Length 1514;
Best Local Similarity 85.7%; Pred. No. 6.2e-240;
Matches 1323; Conservative 0; Mismatches 143; Indels 78; Gaps 17;

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Qy       2335 AGAAGACTGGAGTGGTGTTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTATTCA 2394
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Db          1 AGAAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCA 60

Qy       2395 GCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTA 2454
             |||||||||| ||||| |||||||||||||||||||||||||||||| ||||||||||
Db         61 GCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTA 120

Qy       2455 GGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGG 2514
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Db        121 GGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGG 180

Qy       2515 CATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTG 2574
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        181 CATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTG 240

Qy       2575 CTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATT 2634
             |||||||||||| |||||||| ||||| |||||||| ||||||||||||||||||||||
Db        241 CTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATT 300

Qy       2635 TAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGT 2694
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGT 360

Qy       2695 TCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTT 2754
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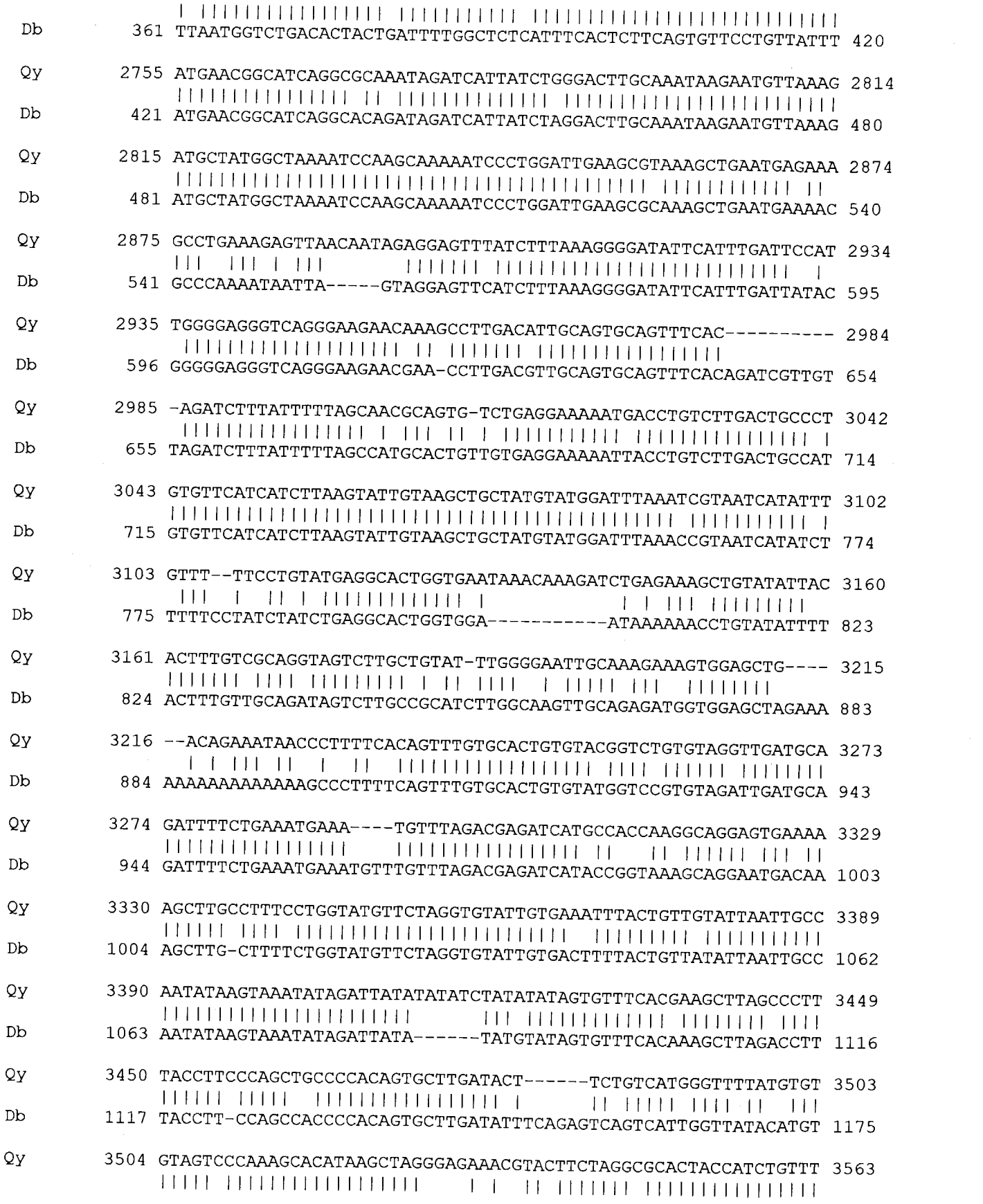

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Db       1176 GTAGTTCCAAAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCATCTGTTT 1235

Qy       3564 TCAACACGAACCGACGCCATGCAAACAGAACTCCTCAACATAAACTTCACTGCACAGACT 3623
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Db       1236 TCAACATGAAATGCC-----ACACACATAGAACTCCAACATCAATTTCATTGCACAGACT 1290

Qy       3624 TACTGTAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA----- 3676
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Db       1291 GACTGTAGTTAATTTTGTCACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTG 1350

Qy       3677 --TGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT--------AAATGACGATTT 3726
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Db       1351 TTTGTTTGCAAATATCAAACATTGTTATGCAAGAAATTATTAATTATAAAATGAAGATTT 1410

Qy       3727 ATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAA 3786
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Db       1411 ATACCATTGTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAA 1470

Qy       3787 AGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAA 3830
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Db       1471 AGCAAAGTATCAATAAAGCTTATAGACGTAAAAAAACTTAGAAA 1514
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RESULT 15
US-10-466-258-10
; Sequence 10, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215)..(814)
US-10-466-258-10

Query Match 25.7%; Score 986; DB 17; Length 1798;
Best Local Similarity 86.1%; Pred. No. 4.5e-239;
Matches 1360; Conservative 0; Mismatches 140; Indels 80; Gaps 21;

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Db        248 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 307

Qy       2364 TTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
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Db        308 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 367

Qy       2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
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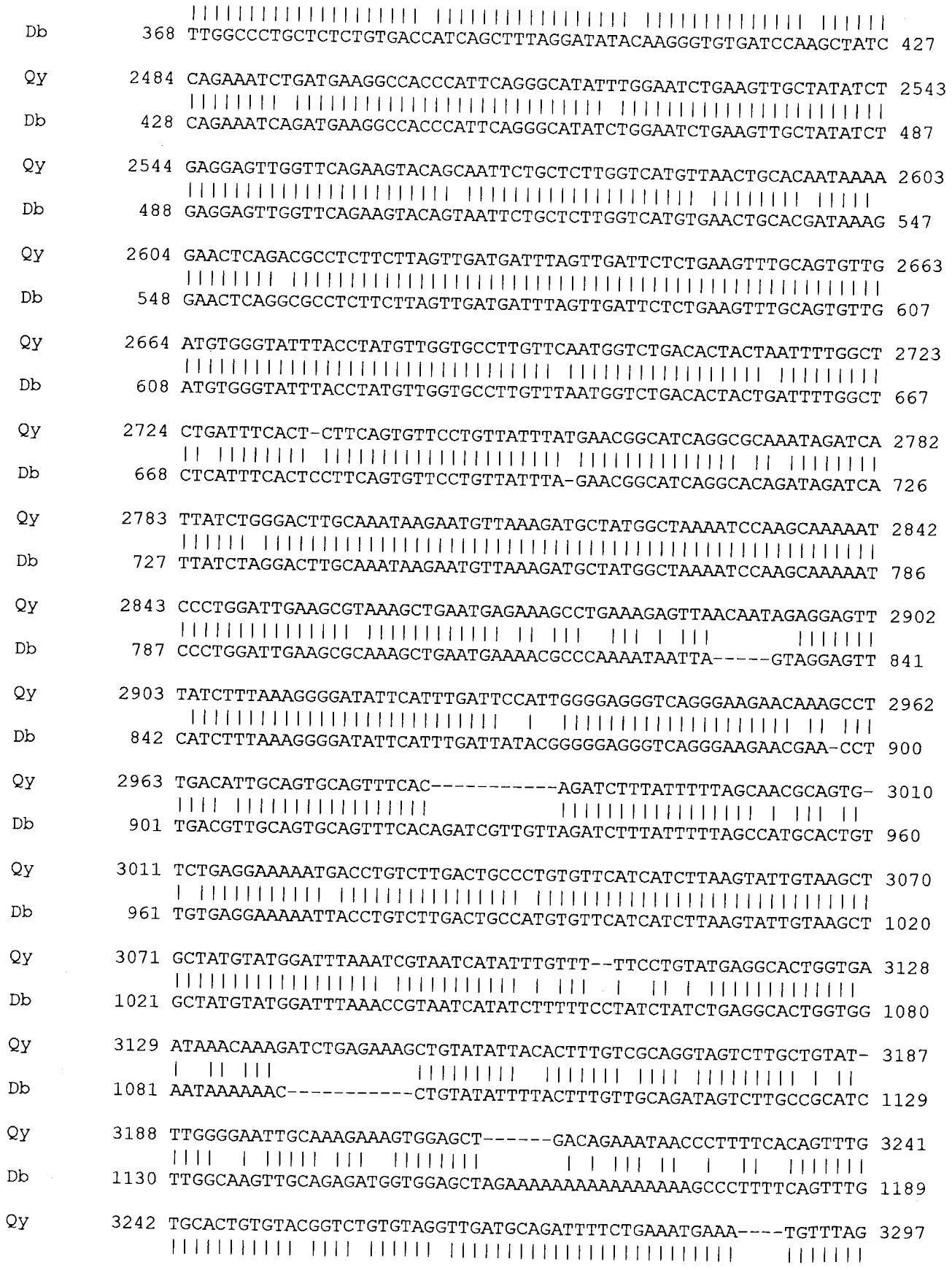

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Db       1250 ACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGT 1308

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Db       1309 GTATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGTAAATATAGATTATA----- 1363

Qy       3418 CTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTG 3477
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Db       1364 -TATGTATAGTGTTTCACAAAGCTTAGACCTTTACCTT-CCAGCCACCCCACAGTGCTTG 1421

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Db       1422 ATATTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAAGA 1481

Qy       3532 AAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAG 3591
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Db       1482 AGAAATATTTCTAGGAGCACTACCATC-GTTTTCAACATGAA---ATGCCACACACATAG 1537

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Db       1538 AACTCCAACAACATCAATTTCATTGCACAGACTGACTGTAGTTAATTTTGTCACAGGATC 1597

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Db       1598 TATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTTTGCAAATATCAAACATTGTTA 1657

Qy       3702 TGTAAGAAAATAT--------AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGA 3753
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Db       1718 ACTAAATCTGTGGAAGGCATTGTAAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGAC 1777

Qy       3814 TTAAAAAAAAAAAAAAAAAA 3833
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Db       1778 CCAAAACGAAAAAAAAAAAA 1797


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Job time : 1639.06 secs
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